

OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:18:36 ; Search time 246.613 Seconds
(without alignments)
7347.063 Million cell updates/sec

Title: US-09-931-157-1
Perfect score: 4105
Sequence: 1 gaattcgcgccgcctcttg.....taaaagtttacagaaacctt 4105

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4105	100.0	4105	4	US-08-121-446-1	Sequence 1, Appli
2	4079	99.4	4079	4	US-09-016-434-1257	Sequence 1257, Ap
3	406.2	9.9	1321	4	US-09-175-658B-20	Sequence 20, Appl
4	395.8	9.6	1470	4	US-09-016-434-1203	Sequence 1203, Ap
5	395.8	9.6	1873	3	US-08-910-864-13	Sequence 13, Appl
6	395.8	9.6	4301	4	US-08-121-446-3	Sequence 3, Appli
7	101.8	2.5	1700	5	PCT-US92-02091-1	Sequence 1, Appli
8	91	2.2	1726	4	US-09-016-434-1215	Sequence 1215, Ap
9	91	2.2	1726	5	PCT-US92-02091-3	Sequence 3, Appli
10	79.6	1.9	1205	3	US-09-120-772-1	Sequence 1, Appli
11	79.6	1.9	1413	4	US-09-016-434-1275	Sequence 1275, Ap

	12	68.6	1.7	1352	4	US-09-016-434-1233	Sequence 1233, Ap
	13	68.6	1.7	1352	5	PCT-US92-02091-7	Sequence 7, Appli
	14	65.8	1.6	1584	5	PCT-US92-02091-5	Sequence 5, Appli
	15	63.6	1.5	1563	1	US-08-279-590A-1	Sequence 1, Appli
	16	63.6	1.5	1563	1	US-08-910-092-1	Sequence 1, Appli
c	17	51.4	1.3	3095	6	5231168-1	Patent No. 5231168
	18	47.4	1.2	1842	4	US-09-170-496D-91	Sequence 91, Appl
	19	47.4	1.2	1842	4	US-09-170-496D-211	Sequence 211, App
	20	46.8	1.1	1238	4	US-09-761-962A-2	Sequence 2, Appli
	21	46.8	1.1	1257	4	US-09-761-962A-5	Sequence 5, Appli
	22	46.8	1.1	1334	4	US-09-761-962A-3	Sequence 3, Appli
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	24	46.8	1.1	1365	4	US-09-761-962A-11	Sequence 11, Appl
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	27	46.8	1.1	1610	4	US-09-761-962A-16	Sequence 16, Appl
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	36	44.8	1.1	1443	3	US-08-959-381A-3	Sequence 3, Appli
	37	44.8	1.1	1446	4	US-09-170-496D-81	Sequence 81, Appl
	38	44.8	1.1	1446	4	US-09-170-496D-207	Sequence 207, App
	39	44.8	1.1	1626	3	US-08-959-381A-4	Sequence 4, Appli
	40	44.2	1.1	1610	3	US-08-889-108-7	Sequence 7, Appli
	41	44.2	1.1	1610	5	PCT-US94-10358-7	Sequence 7, Appli
	42	44.2	1.1	2160	3	US-08-188-275A-1	Sequence 1, Appli
	43	44.2	1.1	2162	4	US-09-351-198-1	Sequence 1, Appli
	44	44.2	1.1	2162	4	US-09-113-426-1	Sequence 1, Appli
	45	44.2	1.1	2162	4	US-09-016-434-1379	Sequence 1379, Ap

ALIGNMENTS

RESULT 1

US-08-121-446-1

; Sequence 1, Application US/08121446

; Patent No. 6313276

; GENERAL INFORMATION:

; APPLICANT: IMURA, HIROO

; APPLICANT: NAKAO, KAZUWA

; APPLICANT: NAKANISHI, SHIGETADA

; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485..1768
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 545
US-08-121-446-1

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Query Match          100.0%; Score 4105; DB 4; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
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Db	1981	TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
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Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
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Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
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Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880

Qy	2881	TTCCCTTTTCCCATATAGGAAAAATAAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCCATATAGGAAAAATAAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTTCTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTTCTGGGGTTT	3000
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Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCCAAGTGAAGTTTGTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGAAGTTTGTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATAATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATAATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAACTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTAACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTAACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTGTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTGTTGGTTGGT	3480
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Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720

Qy 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780
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 Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

RESULT 2

US-09-016-434-1257

; Sequence 1257, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1257:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g219649
US-09-016-434-1257

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Query Match          99.4%; Score 4079; DB 4; Length 4079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      5 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 64
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Db      1 TCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGGAGAC 60

Qy     65 GGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGCGAGCCCTCGCG 124
        |||
Db     61 GGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGCGAGCCCTCGCG 120

Qy    125 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 184
        |||
Db    121 CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC 180

Qy    185 CATCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG 244
        |||
Db    181 CATCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG 240

Qy    245 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 304
        |||
Db    241 TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA 300

Qy    305 GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 364
        |||
Db    301 GCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTCTGGC 360

Qy    365 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 424
        |||
Db    361 CCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAA 420

Qy    425 AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 484
        |||
Db    421 AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG 480

Qy    485 ATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 544

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Db	481	 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540
Qy	545	GATAATCCTGAGAGATA CAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	604
Db	541	 GATAATCCTGAGAGATA CAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
Db	601	 CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	660
Qy	665	AGCAATGGCTCAATGCACAAC TATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	661	 AGCAATGGCTCAATGCACAAC TATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	720
Qy	725	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	721	 TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	 CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGGCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	 AGTCTTGGCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	 CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	 TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTT CAGGGAATTGGGATTCCTTTG	1084
Db	1021	 GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTT CAGGGAATTGGGATTCCTTTG	1080
Qy	1085	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTTATCCTGGCCATTCTTGAA	1144
Db	1081	 GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTTATCCTGGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGT CATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141	 GCGATTGGCTTCGT CATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	 CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	1261	 GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384

Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGACTGG	1924
Db	1861	TTCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2164
Db	2101	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220

Qy	2225	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAGACAAAAATA	2344
Db	2281	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAGACAAAAATA	2340
Qy	2345	GTATTCAAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTAAACAC	2404
Db	2341	GTATTCAAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTAAACAC	2400
Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAATAGATGTTACTCAAAGAAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
Db	2461	GCAGTTTAATAGATGTTACTCAAAGAAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAGTAATGCTTCA	2584
Db	2521	TGTTTTATTACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2644
Db	2581	ATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	TCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
Qy	2945	AATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3004
Db	2941	AATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3064
Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3060

Qy	3065	CACAGTGACTTTTGTCTGGGCATTTTCCCGAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGTCTGGGCATTTTCCCGAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3184
Db	3121	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240
Qy	3245	TGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
Qy	3365	GCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTTCTGAAGGCGTCAACGTGCATTTTATTATATGGACTGGTAAGTAAC	3964

Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4020
Qy	4025	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4083
Db	4021	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4079

Qy 3965 TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA 4024

Db 3961 TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA 4020

Qy 4025 ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAA 4083

Db 4021 ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTGTA 4079

RESULT 3

US-09-175-658B-20

; Sequence 20, Application US/09175658B

; Patent No. 6372900

; GENERAL INFORMATION:

APPLICANT: METALLINOS, DANIKA

APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

; CURRENT APPLICATION NUMBER: US/09/175,658B

; CURRENT FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 60/062,562

PRIOR FILING DATE: 1997-10-21

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 1321

; TYPE: DNA

; ORGANISM: Horse

US-09-175-658B-20

Query Match 9.9%; Score 406.2; DB 4; Length 1321;

Best Local Similarity 67.2%; Pred. No. 1.8e-95:

Matches 630; Conservative 0; Mismatches 283; Indels 24; Gaps 3;

Qy 717 CTTTCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGA 776

Db 310 CTTTCAAGTACATCAACACAGTAGTGTCCTGCCTAGTGTTTCGTGCTGGGCATCATCGGAA 369

Qy 777 ATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGC 836

Db 370 ACTCCACACTGCTGAGAAATCATTTTACAAGAAACAAGTGCATGCGGAACGGGCCCTAATATCT 429

Qy 837 TGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATG 896

Db 430 TGATCGCCAGCCTGGCTCTCCGAGACCTGCTGCAAATCATCATTGACGTCCTCCCATCAATG 488

Qy 897 TATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTT 956

Db 490 TCTACAAGCTGCTGGCTGAGGACTGGCC-----CTTTGGAGTCGAGATGT 534

Qy 957 GCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCG 1016

Db 535 GTAAGCTGGTGCCTTTTCATACAGAAGGCCTCCGTGGGCATCACTGTGCTGAGTCTGTGTG 594

Qy	1017	CTCTTAGTGTGTTGACAGGTCAGAGCAGTTGCTCCTGGAGTCGTGTTTCAGGGAATTGGGA	1076
Db	595	CTCTAAGTATTGACAGATATCGAGCTGTTGCTTCCTTGGAGCGAATTAAAGGAATTCGGG	654
Qy	1077	TTCCTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCA	1136
Db	655	TTCCAAAAATGGACAGCAGTAGAAAAATGTTTAAATTTGGGTGGTCTCTGTGGTTCTGGCTG	714
Qy	1137	TTCCTGAAGCGATTGGCTTCGTCAATGGTACCCCTTTGAATATAGGGGTGAACAGCATAAAA	1196
Db	715	TCCCTGAAGCCGTGGGTTTTGATATGATTACCGCTGACTACAAAGGAAGTTATCTGCGAA	774
Qy	1197	CCTGTATGCTCAATGCCAC-----ATCAAAATTCATGGAGTTCTACCAAGATGTAAAGG	1250
Db	775	TCTGCCCTGCTTCATCCCACTCAGAAAAACAGCCTTCATGCAGTTTTACAAGAAATGCTAAGG	834
Qy	1251	ACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACA	1310
Db	835	ACTGGTGGCTATTTAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATA	894
Qy	1311	CCCTCATGACTTGTGAGATGTTGAACAGAAAGGAATGGCAGCTTGAGAATTGCCCTCAGTG	1370
Db	895	CCTTGATGACCTGTGAAATGTTGAGAAAAGAAGAGTGCGCA---TGCAAAATGCTTTAAATG	951
Qy	1371	AACATCTTAAGCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTG	1430
Db	952	ATCACTTAAAGCAGAGAAGGGAAGTGGCGAAAACAGTATTCTGCCTGGTCTTGTCTTTG	1011
Qy	1431	CTCTTTGCTGGTTCCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAA	1490
Db	1012	CCCTGTGCTGGCTTCCTCTTCACTCAGCAGGATTTTGAAACACACTCTTTATGATCAGA	1071
Qy	1491	TGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTA	1550
Db	1072	ATGATCCCCATAGATGTGAACCTTTTGAGCTTTTGTGGTATTGGACTACATTGGCATCA	1131
Qy	1551	ACTTGGCAACCATGAATTTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAAT	1610
Db	1132	ACATGGCCTCCCTGAATTCTTGCAATTAATCCAATAGCTCTGTATTTGGTGAGCAAAAGAT	1191
Qy	1611	TTAAAAAATGTTTCCAGTCATGCCTCTGCTGCTGCTG	1647
Db	1192	TCAAAAACTGCTTTAAGTCGTGCTTATGCTGCTGGTG	1228

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;   ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;   STREET:    3174 PORTER DRIVE
;   CITY:     PALO ALTO
;   STATE:    CALIFORNIA
;   COUNTRY:  USA
;   ZIP:      94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:   IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:   Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/016,434
;   FILING DATE:  HERewith
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:      Zeller, Karen J.
;   REGISTRATION NUMBER:  37,071
;   REFERENCE/DOCKET NUMBER:  PA-0002 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (650) 855-0555
;   TELEFAX:   (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1203:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:    1470 base pairs
;   TYPE:      nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   IMMEDIATE SOURCE:
;   LIBRARY:   GENBANK
;   CLONE:     g182275
US-09-016-434-1203

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Query Match          9.6%;  Score 395.8;  DB 4;  Length 1470;
Best Local Similarity 65.7%;  Pred. No. 9.7e-93;
Matches 634;  Conservative 0;  Mismatches 307;  Indels 24;  Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
        |||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      314 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTTGC 373

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
        |  |  |||  |  |||| |  |  |||| |  |  |||  |  |  |||  |  |  |||  |
Db      374 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 433

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868
        ||  ||  |||  |  ||  |||| |  |  |||| |  |  ||  |  |  |||| |  |
Db      434 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 493

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
        |  |  |||| |  |  |||| |  |  |||| |  |  |||| |  |  |||| |  |
Db      494 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 549

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Qy	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCG	988
Db	550	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	598
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC	1048
Db	599	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	658
Qy	1049	TCCTGGAGTCGTGTTCAAGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	659	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	718
Qy	1109	ATCTGGATCCTGTCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTTCATGGTACCC	1168
Db	719	ATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	778
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	779	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT	838
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCCTATTTCTGTATG	1282
Db	839	TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG	898
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	899	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG	955
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	956	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1015
Qy	1403	ACAGTTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Db	1016	ACCGTCTTTTGCTGGTCCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG	1075
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1076	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT	1135
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1136	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1195
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1196	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC	1255
Qy	1643	TGCTG 1647	
Db	1256	TGGTG 1260	

RESULT 5

US-08-910-864-13

; Sequence 13, Application US/08910864

; Patent No. 6280931

```

; GENERAL INFORMATION:
;   APPLICANT:  SAKAMOTO, AIJI
;   APPLICANT:  HANAOKA, FUMIO
;   TITLE OF INVENTION:  METHOD FOR SPECIFICALLY AMPLIFYING A cDNA OF AN
EXTREMELY
;   TITLE OF INVENTION:  SMALL QUANTITY
;   NUMBER OF SEQUENCES:  13
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  FISH & RICHARDSON P.C.
;     STREET:    4225 EXECUTIVE SQUARE, SUITE 1400
;     CITY:     LA JOLLA
;     STATE:    CA
;     COUNTRY:  USA
;     ZIP:      92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/910,864
;     FILING DATE:       13-AUG-1997
;     CLASSIFICATION:    435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  JP 216506/1996
;     FILING DATE:       16-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:             HAILE, LISA A.
;     REGISTRATION NUMBER:  38,347
;     REFERENCE/DOCKET NUMBER:  07898/017001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:        619-678-5070
;     TELEFAX:          619-678-5099
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1873 base pairs
;       TYPE:    nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  231..1556
US-08-910-864-13

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Query Match          9.6%;  Score 395.8;  DB 3;  Length 1873;
Best Local Similarity 65.7%;  Pred. No. 1.1e-92;
Matches 634;  Conservative 0;  Mismatches 307;  Indels 24;  Gaps 3;

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Qy      689 TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
        |||| | | | | | | | | | | | | | | | | | | | |
Db      498 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 557

Qy      749 ACTATTTTCATCGTGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
        | | ||| | | ||| | | |||| | | | | | | | | | |
Db      558 CTTGTGTTCTGCTGTTGGGATCATCGGGAATCCACACTTCTGAGAATTATCTACAAGAAC 617

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Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC	868
Db	618	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	677
Qy	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	678	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	733
Qy	929	GATCACAAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTTGAGAAGTCCTCG	988
Db	734	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	782
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	783	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	842
Qy	1049	TCCTGGAGTCGTGTTT CAGGGAATTGGGATTCCTTTGGTA ACTGCCATTGAAATTGTCTCC	1108
Db	843	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	902
Qy	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCTG AAGCGATTGGCTTCGTCATGGTACCC	1168
Db	903	ATTTGGGTGGTCTCTGTGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	962
Qy	1169	TTTGAATATAGGGGTGAACAGCAT AAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	963	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	1022
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Db	1023	TTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTATTTCAGTTTCTATTTCTGCTTG	1082
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1083	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG	1139
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1140	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCA AA	1199
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT	1462
Db	1200	ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG	1259
Qy	1463	ATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1260	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT	1319
Qy	1523	T TACTGCTCATGGATTACATCGGTATTA ACTTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1320	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1379
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAA TTGTTCCAGTCATGCCTCTGCTGC	1642
Db	1380	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAA CTGTTAAGTCATGCTTATGCTGC	1439
Qy	1643	TGCTG	1647

Db || ||
 1440 TGGTG 1444

RESULT 6

US-08-121-446-3

; Sequence 3, Application US/08121446
; Patent No. 6313276
; GENERAL INFORMATION:
; APPLICANT: IMURA, HIROO
; APPLICANT: NAKAO, KAZUWA
; APPLICANT: NAKANISHI, SHIGETADA
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1566

US-08-121-446-3

Query Match 9.6%; Score 395.8; DB 4; Length 4301;
Best Local Similarity 65.7%; Pred. No. 1.7e-92;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

Qy 689 TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Db	505	TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC	564
Qy	749	ACTATTTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC	808
Db	565	CTTGTGTTCGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAAC	624
Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC	868
Db	625	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	684
Qy	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Qy	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCG	988
Db	741	-----ATTTGGAGCTGAGATGTGTAAGCTGCTGCCTTTCATACAGAAAGCCTCC	789
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Qy	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Qy	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCTTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Db	910	ATTTGGGTGGTCTCTGTGGTTCGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT	1029
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Db	1030	TTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAAGTTTCTATTTCTGCTTG	1089
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG	1146
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT	1462
Db	1207	ACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCTTACCTCAGCAGG	1266
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT	1326
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCC	1582

Db 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAAACCA 1386
 QY 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642
 || ||||| ||||| ||||| || ||| ||||| || || ||||| || ||||| ||
 Db 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446
 QY 1643 TGCTG 1647
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 Db 1447 TGGTG 1451

PCT-US92-02091-1

; GENERAL INFORMATION:

APPLICANT: Corjay, Martha H.

APPLICANT: Harkins, Richard N.

NUMBER OF SEQUENCES: 8

ADDRESSEE: Edwin P. Ching

CITY: Alameda

COUNTRY: USA

; COMPUTER READ

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; COMPUTER:  IBM PC compatible

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; OPERATING SYSTEM:  PC-DOS/MS

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;      SOFTWARE:  PatentIn Release #1.0

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: PC

FILING DATE: 19920313

CLASSIFICATION: 435

; PRIOR APPLICATION DATA

APPLICATION NUMBER:

FILING DATE: 24-OCT-1989

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/533,659

FILING DATE: 05-JUN-1990

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: A

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-266-7476

TELEFAX: 415-266-7400

; INFORMATION FOR SEO ID NO: 1:

SEQUENCE CHARACTERISTICS:

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;      LENGTH:  1700 base pairs
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; TYPE: NUCLEIC ACID

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; STRANDEDNESS: double
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;      TOPOLOGY:  linear
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MOLECULE TYPE: cDNA to mRNA

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; CELL LINE: Swiss 3T3
; IMMEDIATE SOURCE:
; LIBRARY: Lambda GT10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 378..1532
PCT-US92-02091-1

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Query Match          2.5%; Score 101.8; DB 5; Length 1700;
Best Local Similarity 49.3%; Pred. No. 2.1e-16;
Matches 308; Conservative 0; Mismatches 302; Indels 15; Gaps 1;

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Qy      714 CAGCTTTCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGAATGGTGG 773
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      490 CGGGCTTCATCTATGTCATCCCTGCAGTTTATGGGCTTATCATCGTGATAGGTCTTATTG 549

Qy      774 GGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACG 833
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      550 GCAACATCACGCTCATCAAGATCTTCTGCACGGTCAAGTCCATGCGAAACGTGCCAAACC 609

Qy      834 CGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCA 893
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      610 TGTTTCATCTCTAGCCTGGCTTTGGGAGACCTGCTGCTGCTGGTGACATGCGCCCCTGTGG 669

Qy      894 ATGTATTTAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTTC 953
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      670 ATGCCAGCAAGTACCTGGCTGACAGGTGGCTA-----TTTGGCAGAATTG 714

Qy      954 TTTGCAAGCTGTTCCCTTTTTTGCAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCT 1013
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      715 GCTGCAAACTGATCCCCTTTATACAACTTACTTCAGTGGGGGTGTCTGTCTTCACACTTA 774

Qy      1014 GCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTG 1073
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      775 CGGCACTGTGAGCTGACAGGTACAAAGCCATTGTACGGCCAATGGATATCCAGGCATCCC 834

Qy      1074 GGATTCCTTTGGTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGG 1133
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      835 ATGCCCTGATGAAGATCTGTCTCAAAGCTGCTTTGATCTGGATTGTCTCTATGTTGTTGG 894

Qy      1134 CCATTCCTGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATA 1193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      895 CCATCCCAGAGGCTGTGTTTTCTGACCTCCACCCCTTCCATGTGAAAGATACCAACCAA 954

Qy      1194 AAACCTGTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACT 1253
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      955 CCTTCATTAGTTGTGCCCCCTACCCACACTCCAATGAGCTACACCCTAAAATCCATTCCA 1014

Qy      1254 GGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCC 1313
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1015 TGGCTTCCTTTCTGGTTTTCTACGTTATCCCACTGGCGATCATCTCTGTCTACTACTACT 1074

Qy      1314 TCATGACTTGTGAGATGTTGAACAG 1338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 1075 TCATTGCCCCGAAATCTGATTGAG 1099

RESULT 8

US-09-016-434-1215

; Sequence 1215, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g183649

US-09-016-434-1215

Query Match 2.2%; Score 91; DB 4; Length 1726;
Best Local Similarity 48.3%; Pred. No. 1.3e-13;
Matches 299; Conservative 0; Mismatches 305; Indels 15; Gaps 1;

Qy 720 TCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATG 779
|| || | | || | | | || | | | || | | | ||

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Db      514 TCCTCTATGTCATCCCTGCAGTTTATGGGGTTATCATTCTGATAGGCCTCATTGGCAACA 573
Qy      780 CAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGA 839
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      574 TCACTTTGATCAAGATCTTCTGTACAGTCAAGTCCATGCGAAACGTTCCAAACCTGTTCA 633
Qy      840 TAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTAT 899
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCCTCCTAATAACGTGTGCTCCAGTGGATGCCA 693
Qy      900 TTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 959
      | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGC-----TGCA 738
Qy      960 AGCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTC 1019
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      739 AACTGATCCCTTTATACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACACTCACGGCGC 798
Qy      1020 TTAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTC 1079
      | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      799 TCTCGGCAGACAGATACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCTCCCATGCCC 858
Qy      1080 CTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTC 1139
      || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      859 TGATGAAGATCTGCCTCAAAGCCGCCTTTATCTGGATCATCTCCATGCTGCTGGCCATTC 918
Qy      1140 CTGAAGCGATTGGCTTCGTCAATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCT 1199
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      919 CAGAGGCCGTGTTTTCTGACCTCCATCCCTTCCATGAGGAAAGCACCAACCAGACCTTCA 978
Qy      1200 GTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGC 1259
      || | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      979 TTAGCTGTGCCCCATACCCCACTCTAATGAGCTTCACCCCAAATCCATTCTATGGCTT 1038
Qy      1260 TCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGA 1319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1039 CCTTTCTGGTCTTCTACGTATCCCACTGTGATCATCTCTGTTTACTACTACTTCATTG 1098
Qy      1320 CTTGTGAGATGTTGAACAG 1338
      || | ||| ||| ||| ||| |||
Db      1099 CTAAAAATCTGATCCAGAG 1117

```

RESULT 9

PCT-US92-02091-3

; Sequence 3, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

```

; STATE: CA
; COUNTRY: USA
; ZIP: 94501
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02091
; FILING DATE: 19920313
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/426,150
; FILING DATE: 24-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/533,659
; FILING DATE: 05-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34090
; REFERENCE/DOCKET NUMBER: A-0092C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-266-7476
; TELEFAX: 415-266-7400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1726 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Small cell lung carcinoma
; CELL LINE: NCI-H345
; IMMEDIATE SOURCE:
; LIBRARY: Lambda GT10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 399..1553
PCT-US92-02091-3

```

```

Query Match          2.2%; Score 91; DB 5; Length 1726;
Best Local Similarity 48.3%; Pred. No. 1.3e-13;
Matches 299; Conservative 0; Mismatches 305; Indels 15; Gaps 1;

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Qy      720 TCAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATG 779
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      514 TCCTCTATGTCATCCCTGCAGTTTATGGGGTTATCATTCTGATAGGCCTCATTGGCAACA 573

Qy      780 CAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGA 839
          ||| || ||| |||| ||  ||  ||| ||| ||| ||| ||| |||
Db      574 TCACTTTGATCAAGATCTTCTGTACAGTCAAGTCCATGCGAAACGTTCCAAACCTGTTCA 633

Qy      840 TAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTAT 899

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      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCCTCCTAATAACGTGTGCTCCAGTGGATGCCA 693
Qy      900 TTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 959
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGC-----TGCA 738
Qy      960 AGCTGTTCCCTTTTTCGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTC 1019
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      739 AACTGATCCCCTTTATACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACACTCACGGCGC 798
Qy      1020 TTAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACAGGAATTGGGATTC 1079
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      799 TCTCGGCAGACAGATACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCTCCCATGCCC 858
Qy      1080 CTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTC 1139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      859 TGATGAAGATCTGCCTCAAAGCCGCCTTTATCTGGATCATCTCCATGCTGCTGGCCATTC 918
Qy      1140 CTGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCT 1199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      919 CAGAGGCCGTGTTTTCTGACCTCCATCCCTTCCATGAGGAAAGCACCAACCAGACCTTCA 978
Qy      1200 GTATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGC 1259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      979 TTAGCTGTGCCCCATACCCCACTCTAATGAGCTTCACCCCAAATCCATTCTATGGCTT 1038
Qy      1260 TCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGA 1319
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1039 CCTTTCTGGTCTTCTACGTCACTCCACTGTGATCATCTCTGTTTACTACTACTTCATTG 1098
Qy      1320 CTTGTGAGATGTTGAACAG 1338
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1099 CTAAAAATCTGATCCAGAG 1117

```

RESULT 10

US-09-120-772-1

; Sequence 1, Application US/09120772

; Patent No. 6143521

; GENERAL INFORMATION:

; APPLICANT: LANE, PAMELA

; APPLICANT: TSUI, PING

; APPLICANT: ELSHOURBAGY, NABIL

; TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE

; TITLE OF INVENTION: 3

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ratner & Prestia

; STREET: P.O. Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

```

;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/120,772
;      FILING DATE:  22-JUL-1998
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Prestia, Paul F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GP-70505
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0700
;      TELEX:  846169
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  1205 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
US-09-120-772-1

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```

Query Match          1.9%;  Score 79.6;  DB 3;  Length 1205;
Best Local Similarity 46.9%;  Pred. No. 9.9e-11;
Matches 419;  Conservative 0;  Mismatches 439;  Indels 36;  Gaps 4;

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```

Qy      761 GTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGG 820
      ||||| || | || ||||| || | || | || || || || || || ||
Db      180 GTGGGCATCCTTGGAATGCTATTCTCATCAAAGTCTTTTTCAAGACCAAATCCATGCAA 239

Qy      821 AATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATT 880
      | | | || | | | | | | | | | | | | | | | | | | | | | |
Db      240 ACAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACT 299

Qy      881 GATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGAC 940
      | | || | | || | | | | | | | | | | | | | | | |
Db      300 TGTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTC----- 347

Qy      941 TTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACC 1000
      || | | | | | | | | | | | | | | | | | | | | | |
Db      348 ---GGAAGAATTGGTTGTAAGGTGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCA 404

Qy      1001 GTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGT 1060
      || ||| | | || | | | | | | | | | | | | | | |
Db      405 GTGTTACATTAGCAATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAG 464

Qy      1061 GTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTG 1120
      ||| | | | | | | | | | | | | | | | | | | | |
Db      465 CGACAGCCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTG 524

Qy      1121 TCCTTTATCCTGGCCATTTCCTGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGG 1180
      || | | | | | | | | | | | | | | | | | | | | |
Db      525 TCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCC 584

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Qy 1181 GGTGAACAGCATAAACCTGTATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAA 1240
 | | | | | | | | | | | | | | | | | | | | | |
 Db 585 AATAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAA 644

Qy 1241 GATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCG 1300
 | | | | | | | | | | | | | | | | | | | | | |
 Db 645 GAAATACATTCTCTGCTGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCT 704

Qy 1301 ATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATT 1360
 | | | | | | | | | | | | | | | | | | | | | |
 Db 705 GTCTACTATTCTTGATTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAG 764

Qy 1361 GCCCTCAGTGAACATCTTAAGCAG-----CGTCGAGAAGTGGCAAAAACAGTTTTTC 1411
 | | | | | | | | | | | | | | | | | | | | | |
 Db 765 GAACAAAGCCATGCCCGTAAGCAGATTGAATCCCGAAAGAGAATTGCCGAAACGGTATTG 824

Qy 1412 TGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGTATATTGAAG 1471
 | | | | | | | | | | | | | | | | | | | | | |
 Db 825 GTGTTGGTGGCTCTGTTTGGCCTCTGCTGGTTGCCAAATCACCT--CCTGTACCTCTACC 882

Qy 1472 AAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC 1531
 | | | | | | | | | | | | | | | | | | | | | |
 Db 883 ATTCATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCACTTTTACCATT- 941

Qy 1532 ATGGATTACATCGGTATTAAGTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTG 1591
 | | | | | | | | | | | | | | | | | | | | | |
 Db 942 -----TTCTCTCGGGTTTTGGCTTTTCTAGCAATTCTTGCCTAAACCCCTTTGCTCTC 992

Qy 1592 TATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGC 1645
 | | | | | | | | | | | | | | | | | | | | | |
 Db 993 TACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGC 1046

RESULT 11

US-09-016-434-1275

; Sequence 1275, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1275:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g291876
US-09-016-434-1275

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Query Match          1.9%; Score 79.6; DB 4; Length 1413;
Best Local Similarity 46.9%; Pred. No. 1.1e-10;
Matches 419; Conservative 0; Mismatches 439; Indels 36; Gaps 4;

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Qy      761 GTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGG 820
      ||||| || | || ||||| | || | || | || | ||||| |||
Db      327 GTGGGCATCCTTGGAAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 386

Qy      821 AATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATT 880
      | | | || | | | | || | || | || | ||||| || | | | | |
Db      387 ACAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACT 446

Qy      881 GATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGAC 940
      | | || | | || | | | | || | || | | ||||| ||
Db      447 TGTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTC----- 494

Qy      941 TTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACC 1000
      || | || | || | || | || | || | || | || | || | |
Db      495 ---GGAAGAATTGGTTGTAAGGTGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTCA 551

Qy      1001 GTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGT 1060
      || ||| | | || | || | ||||| |||| | ||||| |
Db      552 GTGTTACATTAACAATTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAG 611

Qy      1061 GTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTG 1120
      ||| | | || | || | || | || | || | ||||| ||
Db      612 CGACAGCCCTCCAATGCCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTG 671

Qy      1121 TCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGG 1180
      || | || | || | ||||| || | | | | | || | || |
Db      672 TCTATGATATTTGCTCTACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCC 731

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Qy 1181 GGTGAACAGCATAAAACCTGTATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAA 1240
 | | | | | | | | | | | | | | | | | |
 Db 732 AATAAAAATATGACATTTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAA 791

Qy 1241 GATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCG 1300
 | | | | | | | | | | | | | | | | | |
 Db 792 GAAATACATTCTCTGCTGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCT 851

Qy 1301 ATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATT 1360
 | | | | | | | | | | | | | | | | | |
 Db 852 GTCTACTATTCTTGATTGCTAGGACCCCTTTACAAAAGCACCTGAACATACCTACTGAG 911

Qy 1361 GCCCTCAGTGAACATCTTAAGCAG-----CGTCGAGAAGTGGCAAAAACAGTTTTTC 1411
 | | | | | | | | | | | | | | | | | |
 Db 912 GAACAAAGCCATGCCCGTAAGCAGATTGAATCCCGAAAGAGAATTGCCGAAACGGTATTG 971

Qy 1412 TGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGTATATTGAAG 1471
 | | | | | | | | | | | | | | | | | |
 Db 972 GTGTTGGTGGCTCTGTTTGCCCTCTGCTGGTTGCCAAATCACCT--CCTGTACCTCTACC 1029

Qy 1472 AAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC 1531
 | | | | | | | | | | | | | | | | | |
 Db 1030 ATTCATTCACTTCTCAAACCTATGTAGACCCCTCTGCCATGCATTTTCACTTTTACCATT- 1088

Qy 1532 ATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTG 1591
 | | | | | | | | | | | | | | | | | |
 Db 1089 -----TTCTCTCGGGTTTGGCTTTCAGCAATTCTTGCGTAAACCCCTTTGCTCTC 1139

Qy 1592 TATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGC 1645
 | | | | | | | | | | | | | | | | | |
 Db 1140 TACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGC 1193

RESULT 12

US-09-016-434-1233

; Sequence 1233, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

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; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g189241
US-09-016-434-1233

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```

Query Match          1.7%; Score 68.6; DB 4; Length 1352;
Best Local Similarity 50.1%; Pred. No. 7.6e-08;
Matches 210; Conservative 0; Mismatches 194; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACAGAACAAA 811
      || ||| ||||| || ||||| || | ||| | ||||| | |||
Db      296 ATCATCACCGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATCTTCATCACCAACAGC 355

Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATCTAT 871
      ||||| || ||||| || || | | ||| || ||||| |
Db      356 GCCATGAGGAGCGTCCCCAACATCTTCATCTCTAACCTGGCGGCCGGGACTTGCTGCTG 415

Qy      872 GTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGAT 931
      || ||| |||| | || | || ||| || ||||| || ||
Db      416 CTGCTCACCTGCGTCCC-----GGTGGACGCCTCGCGCTACTTCTTCGAC 460

Qy      932 CACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCGGTG 991
      | ||||| | ||||| || ||||| | ||||| | |||||
Db      461 GAGTGGATGTTTGGCAAGGTGGGCTGCAAACTGATCCCTGTTCATCCAGCTCACTTCCGTG 520

Qy      992 GGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCCTCC 1051
      ||| | |||| || || || || || ||||| ||||| |||
Db      521 GGGGTTTCCGTGTTCACTCTCACTGCCCTCAGCGCCGACAGGTACAGAGCCATCGTTAAC 580

Qy      1052 TGGAGTCGTGTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCCATC 1111
      | || | |||| || || || || || ||||| ||||| |||
Db      581 CCCATGGACATGCAGACGTCAGGGGCATTGCTGCGGACCTGTGTGAAGGCCATGGGTATC 640

Qy      1112 TGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCCTT 1170
      ||| | |||| | ||||| ||||| ||||| | ||| |||
Db      641 TGGGTGGTCTCCGTGTTGCTGGCAGTTCCTGAAGCGGTGTTTTCAGAAGTGGCTCGCAT 699

```

```

RESULT 13
PCT-US92-02091-7
; Sequence 7, Application PC/TUS9202091
; GENERAL INFORMATION:
;   APPLICANT:  Battey Jr., James F.
;   APPLICANT:  Corjay, Martha H.
;   APPLICANT:  Feldman, Richard I.
;   APPLICANT:  Harkins, Richard N.
;   TITLE OF INVENTION:  RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
;   NUMBER OF SEQUENCES:  8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Edwin P. Ching
;     STREET:    1501 Harbor Bay Parkway
;     CITY:      Alameda
;     STATE:     CA
;     COUNTRY:   USA
;     ZIP:       94501
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US92/02091
;     FILING DATE:        19920313
;     CLASSIFICATION:     435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/426,150
;     FILING DATE:        24-OCT-1989
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/533,659
;     FILING DATE:        05-JUN-1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME:              Ching, Edwin P.
;     REGISTRATION NUMBER: 34090
;     REFERENCE/DOCKET NUMBER: A-0092C
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:         415-266-7476
;     TELEFAX:           415-266-7400
;   INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1352 base pairs
;       TYPE:   NUCLEIC ACID
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;       CELL TYPE: Small cell lung carcinoma
;       CELL LINE: NCI-H345
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  140..1312
PCT-US92-02091-7

Query Match                1.7%;  Score 68.6;  DB 5;  Length 1352;

```

Best Local Similarity 50.1%; Pred. No. 7.6e-08;
Matches 210; Conservative 0; Mismatches 194; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAACAA 811
      || ||| ||||| || ||||| || | ||| | ||||| | | |||
Db      296 ATCATCACCGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATCTTCATCACCAACAGC 355

Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTAT 871
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Db      356 GCCATGAGGAGCGTCCCCAACATCTTCATCTCTAACCTGGCGGCCGGGACTTGCTGCTG 415

Qy      872 GTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTTGAT 931
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Db      416 CTGCTCACCTGCGTCCC-----GGTGGACGCCTCGCGCTACTTCTTCGAC 460

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Db      461 GAGTGGATGTTTGGCAAGGTGGGCTGCAAACTGATCCCTGTCATCCAGCTCACTTCCGTG 520

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Db      521 GGGGTTTCCGTGTTCACTCTCACTGCCCTCAGCGCCGACAGGTACAGAGCCATCGTTAAC 580

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Db      581 CCCATGGACATGCAGACGTGAGGGGCATTGCTGCGGACCTGTGTGAAGGCCATGGGTATC 640

Qy      1112 TGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTATGGTACCCTT 1170
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RESULT 14

PCT-US92-02091-5

; Sequence 5, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02091

; FILING DATE: 19920313

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/426,150
; FILING DATE: 24-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/533,659
; FILING DATE: 05-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34090
; REFERENCE/DOCKET NUMBER: A-0092C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-266-7476
; TELEFAX: 415-266-7400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; TISSUE TYPE: Esophagus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 132..1304
PCT-US92-02091-5

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Query Match          1.6%; Score 65.8; DB 5; Length 1584;
Best Local Similarity 49.6%; Pred. No. 4.4e-07;
Matches 209; Conservative 0; Mismatches 197; Indels 15; Gaps 1;

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Qy      752 ATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTCACAGAACAAA 811
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Qy      812 TGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATCTAT 871
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Db      408 CTGCTGACCTGCGTCCCAGTGGATGCCTCC-----CGATACTTCTTTGAT 452

Qy      932 CACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCGGTG 991
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Qy      1052 TGGAGTCGTGTTCAGGGAATTGGGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCCATC 1111
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RESULT 15

US-08-279-590A-1

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; Sequence 1, Application US/08279590A
; Patent No. 5656749
; GENERAL INFORMATION:
;   APPLICANT: ELIOT R. SPINDEL, SRINIVASA
;   APPLICANT: NAGALLA AND BRENDA BARRY
;   TITLE OF INVENTION: NUCLEIC ACIDS ENCODING
;   TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE
;   TITLE OF INVENTION: PEPTIDES
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: U.S.A.
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;     COMPUTER: IBM PS/2 Model 50Z or 55SX
;     OPERATING SYSTEM: MS-DOS (Version 5.0)
;     SOFTWARE: WordPerfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/279,590A
;     FILING DATE: July 22, 1994
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: No. 5656749e
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Y. Rocky Tsao
;     REGISTRATION NUMBER: 34,053
;     REFERENCE/DOCKET NUMBER: 00537/098001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 542-5070
;     TELEFAX: (617) 542-8906
;     TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1563
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
US-08-279-590A-1

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Query Match 1.5%; Score 63.6; DB 1; Length 1563;

Best Local Similarity 45.5%; Pred. No. 1.6e-06;
Matches 332; Conservative 0; Mismatches 374; Indels 24; Gaps 2;

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Qy      735 CTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGA 794
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Qy      915 GGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTT 974
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Qy      1386 GTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTGTGAATTTTGTCTCTTTGCTGGTTCC 1445
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Db      985 GCAAACGAGTGGCAAAAACAGTTTGGTGTGGTGGCATTGTTGCGAGTGTGCTGGTTGC 1044

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Job time : 254.613 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 10:54:32 ; Search time 1202.3 Seconds
(without alignments)
11347.756 Million cell updates/sec

Title: US-09-931-157-1
Perfect score: 4105
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	4105	100.0	4105	9	US-09-931-157-1	Sequence 1, Appli
2	4105	100.0	4105	13	US-10-007-926A-229	Sequence 229, App
3	4105	100.0	4105	13	US-10-101-510-370	Sequence 370, App
4	4105	100.0	4105	15	US-10-225-567A-115	Sequence 115, App
5	2470	60.2	2595	10	US-09-919-497-12	Sequence 12, Appl
6	2470	60.2	2595	13	US-10-204-752-30	Sequence 30, Appl
7	1280.8	31.2	1284	13	US-09-826-509-494	Sequence 494, App
8	521	12.7	560	13	US-10-101-510-59	Sequence 59, Appl
9	412.4	10.0	451	11	US-09-918-995-8960	Sequence 8960, Ap
10	395.8	9.6	4286	13	US-10-007-926A-177	Sequence 177, App
11	395.8	9.6	4286	13	US-09-921-406C-13	Sequence 13, Appl
12	395.8	9.6	4286	13	US-10-210-120-15	Sequence 15, Appl
13	395.8	9.6	4286	15	US-10-225-567A-113	Sequence 113, App
14	395.8	9.6	4301	9	US-09-931-157-2	Sequence 2, Appli
15	392.6	9.6	1329	13	US-09-826-509-496	Sequence 496, App
16	284.4	6.9	438	10	US-09-867-701-3320	Sequence 3320, Ap
c 17	155	3.8	170	13	US-10-007-926A-228	Sequence 228, App
c 18	147	3.6	592	9	US-09-962-436-531	Sequence 531, App
c 19	147	3.6	592	10	US-09-880-107-2060	Sequence 2060, Ap
c 20	147	3.6	592	10	US-09-954-531-917	Sequence 917, App
21	114.6	2.8	800	9	US-09-778-927A-27	Sequence 27, Appl
c 22	101	2.5	183337	15	US-10-020-141-5	Sequence 5, Appli
23	100	2.4	101	13	US-09-998-904-6	Sequence 6, Appli
24	91	2.2	1155	13	US-09-826-509-510	Sequence 510, App
25	91	2.2	1726	15	US-10-225-567A-129	Sequence 129, App
26	79.6	1.9	1413	15	US-10-225-567A-57	Sequence 57, Appl
27	78	1.9	1200	13	US-09-826-509-458	Sequence 458, App
28	68.6	1.7	1173	13	US-09-826-509-530	Sequence 530, App
29	68.6	1.7	1352	13	US-10-116-275-210	Sequence 210, App
30	68.6	1.7	1352	15	US-10-225-567A-198	Sequence 198, App
31	68.4	1.7	2595	9	US-09-160-116-11	Sequence 11, Appl
32	62.8	1.5	3673778	13	US-10-312-841-1	Sequence 1, Appli
33	62	1.5	1563	9	US-09-160-116-1	Sequence 1, Appli
c 34	61.6	1.5	316	13	US-10-029-386-26963	Sequence 26963, A
c 35	61.6	1.5	566	13	US-10-029-386-13263	Sequence 13263, A
36	60	1.5	60	13	US-09-908-975-14863	Sequence 14863, A
37	57	1.4	65	13	US-09-908-975-29571	Sequence 29571, A
38	57	1.4	5145	13	US-10-311-455-321	Sequence 321, App
39	57	1.4	5145	13	US-10-240-485-17	Sequence 17, Appl
c 40	56.4	1.4	18624	13	US-10-311-455-1675	Sequence 1675, Ap
41	56.2	1.4	99116	13	US-10-298-122-1	Sequence 1, Appli
42	56	1.4	15548	13	US-10-311-455-2128	Sequence 2128, Ap
43	56	1.4	16766	13	US-10-311-455-2130	Sequence 2130, Ap
44	56	1.4	17491	13	US-10-240-485-127	Sequence 127, App
45	55.6	1.4	11015	13	US-10-204-708-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1

US-09-931-157-1

; Sequence 1, Application US/09931157

; Patent No. US20020082414A1

; GENERAL INFORMATION:

; APPLICANT: Imura, Hiroo

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; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4105
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (485)...(1768)
; NAME/KEY: sig_peptide
; LOCATION: (485)...(544)
; NAME/KEY: mat_peptide
; LOCATION: (545)...(1768)
US-09-931-157-1

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Query Match          100.0%; Score 4105; DB 9; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC 300
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Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
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Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
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Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
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Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
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Qy	1201	TATGCTCAATGCCACATCAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
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Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100

Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTTAAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTTAAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCACGTCCTACTATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCACGTCCTACTATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAAATGTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000

Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	 TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840

Db	3781	CATCATATGTCAGTGCATATATATGCCTATAAATATAAGCCATAGGTTTCACACCATTTTGTGTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

US-10-007-926A-229

; Sequence 229, Application US/10007926A

; GENERAL INFORMATION:

APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007,926A

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 60/254,090

; PRIOR FILING DATE: 2000-12-08

; NUMBER OF SEQ ID NOS: 468

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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 229

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; LENGTH: 4105
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; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: endothelin receptor type a (EDNRA) gene.

Query Match 100.0%; Score 4105; DB 13; Length 4105;

Best Local Similarity 100.0%; Pred. No. 0;

Qy 1 GAATTTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

[illegible]

Db	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCGAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCGAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900

Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740

Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAA	2400
Db	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640

Db	2581	 TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	 AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	 TCAGTGCCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	 ATGATTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	 CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCTAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480

Db 3421 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT 3480
 Qy 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540
 Qy 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600
 Qy 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3601 TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660
 Qy 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720
 Qy 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780
 Qy 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCAACCATTGTTTGTAG 3840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCAACCATTGTTTGTAG 3840
 Qy 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
 Qy 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
 Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
 Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
 Qy 4081 TAAATATAAAGTTTACAGAAACCTT 4105
 ||||||||||||||||||
 Db 4081 TAAATATAAAGTTTACAGAAACCTT 4105

RESULT 3

US-10-101-510-370

; Sequence 370, Application US/10101510

; Publication No. US20030148295A1

; GENERAL INFORMATION:

; APPLICANT: WAN, JACKSON

; APPLICANT: WANG, YIXIN

; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE

; FILE REFERENCE: 15117.0012

; CURRENT APPLICATION NUMBER: US/10/101,510

; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 370
; LENGTH: 4105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-370

Query Match 100.0%; Score 4105; DB 13; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60
      |||
Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGTCGAGCCCT 120
      |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGTCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||
Db    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC 300
      |||
Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
      |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
      |||
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Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACCTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACCTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500

Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501		
Qy	1561	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1561		
Qy	1621	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1621		
Qy	1621	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1621		
Qy	1681	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1681		
Qy	1681	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1681		
Qy	1741	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Db	1741		
Qy	1741	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Db	1741		
Qy	1801	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1801		
Qy	1801	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1801		
Qy	1861	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1861		
Qy	1861	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1861		
Qy	1921	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1921		
Qy	1921	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1921		
Qy	1981	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1981		
Qy	1981	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1981		
Qy	2041	TTCTGCGTGTTGTATTGAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	2041		
Qy	2041	TTCTGCGTGTTGTATTGAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	2041		
Qy	2101	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2101		
Qy	2101	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2101		
Qy	2161	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2161		
Qy	2161	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2161		
Qy	2221	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTTCAGCCAAACACA	2220
Db	2221		
Qy	2221	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTTCAGCCAAACACA	2220
Db	2221		
Qy	2281	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2281		
Qy	2281	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2281		
Qy	2341	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2341		
Qy	2341	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2341		

Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCCAAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTG	4080

Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAATATAAAGTTTACAGAAACCTT 4105

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Db 4081 TAAATATAAAGTTTACAGAAACCTT 4105

RESULT 4

US-10-225-567A-115

; Sequence 115, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 115

; LENGTH: 4105

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-115

Query Match 100.0%; Score 4105; DB 15; Length 4105;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

||||||||||||||||||||||||||||||||

Db 1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCT 120

||||||||||||||||||||||||||||||||

Db 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCT 120

Qy 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

||||||||||||||||||||||||||||||||

Db 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

||||||||||||||||||||||||||||||||

Db 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy 241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

||||||||||||||||||||||||||||||||

Db 241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy 301 CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC 360

||||||||||||||||||||||||||||||||

Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTTCAGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200

Qy	1201	TATGCTCAATGCCACATCAAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAAATTTTGTCTTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAAATTTTGTCTTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040

Qy	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCACAAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAAACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTTGAAGTGGCCAGATGAGTTTATCATGTCA	2940

Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCAATTGTCACCATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCAATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCCAAGTACTTTTGTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCCAAGTACTTTTGTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	 AAAATCTTTTACTAGTGTGTGTGTATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	 TGTAGCAACCTTCTGCATTCTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	 CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Db	3601	 TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	 ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAACTACTGCCCTTTTGTGTGTTAGCAGTCAAACTATTATTCCACTGGCG	3780

Db 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780

Qy 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840
 |||

Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840

Qy 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
 |||

Db 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900

Qy 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
 |||

Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960

Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
 |||

Db 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020

Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
 |||

Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAAATAAAAGTTTACAGAAACCTT 4105
 |||

Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

RESULT 5

US-09-919-497-12

; Sequence 12, Application US/09919497

; Patent No. US20020106662A1

; GENERAL INFORMATION:

; APPLICANT: Mutter, George L.

; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

; FILE REFERENCE: B0801/7225

; CURRENT APPLICATION NUMBER: US/09/919,497

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/221,735

; PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 2595

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-919-497-12

Query Match 60.2%; Score 2470; DB 10; Length 2595;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1624 CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 1683
 |||

Db 15 CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 74

Qy 1684 GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG 1743
 |||

Db	75	GAACGGAACAAGCATCCAGTGGGAAGAACCCACGATCAAAAACAACCACAACACAGACCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	1863
Db	195	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	254
Qy	1864	CTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	1923
Db	255	CTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	314
Qy	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	2043
Db	375	TGCGTGTTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAAGAGCTTTCAAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAAGAGCTTTCAAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCCTATTTATTTTTTTAAAACA	794
Qy	2404	CAAAATCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAAATCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	915	GTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	974

Qy	2584	AATCAGATAGTTCTTTTTTCACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTCACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTTGATCATT	2883
Db	1214	CTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTTGATCATT	1273
Qy	2884	CCTTTTCCATATAGGAAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACTTGTCAACCATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACTTGTCAACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACTGT	1753
Qy	3364	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813

Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353
Qy	3964	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	4023
Db	2354	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA	4083
Db	2414	AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA	2473
Qy	4084	AATAAAAGTTTACAGAAACCTT	4105
Db	2474	AATAAAAGTTTACAGAAACCTT	2495

RESULT 6

US-10-204-752-30

; Sequence 30, Application US/10204752

; Publication No. US20030152956A1

; GENERAL INFORMATION:

; APPLICANT: OHTANI, No. US20030152956A1iko

; APPLICANT: MATSUI, Keiko

; APPLICANT: YOSHIDA, Nei

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; APPLICANT:  SUGITA, Yuji
; APPLICANT:  IZUHARA, Kenji
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SHZ-009US
; CURRENT APPLICATION NUMBER: US/10/204,752
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: JP 2000-396166
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-752-30

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Query Match          60.2%; Score 2470; DB 13; Length 2595;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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```

Qy      1624 CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 1683
          |||
Db      15   CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT 74

Qy      1684 GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG 1743
          |||
Db      75   GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG 134

Qy      1744 CAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCATAAT 1803
          |||
Db      135  CAGCCATAAGGACAGCATGAACTGACCACCCCTTAGAAGCACTCCTCGGTACTCCCATAAT 194

Qy      1804 CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT 1863
          |||
Db      195  CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT 254

Qy      1864 CTTCTTAATTCACTCCACACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 1923
          |||
Db      255  CTTCTTAATTCACTCCACACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG 314

Qy      1924 GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC 1983
          |||
Db      315  GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC 374

Qy      1984 TGC GTGTTGTATT CAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA 2043
          |||
Db      375  TGC GTGTTGTATT CAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA 434

Qy      2044 TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA 2103
          |||
Db      435  TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA 494

Qy      2104 GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA 2163
          |||
Db      495  GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA 554

Qy      2164 TTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA 2223

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Db	555	 TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	 TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	 TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTTAAACA	2403
Db	735	 AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	 CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	 AATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	 GTGCACTGTATATAGAAGTCTAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTTC	2883
Db	1214	 CTCCTATTCTCTTAATTTTTGTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	 AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063

Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTATATATAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCATATTTTAGGACAGGTAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	2293


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Qy      3904 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 3963
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2294 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 2353

Qy      3964 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413

Qy      4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA 4083
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTA 2473

Qy      4084 AATAAAAGTTTACAGAAACCTT 4105
        ||||||||||||||||||
Db      2474 AATAAAAGTTTACAGAAACCTT 2495

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RESULT 7

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US-09-826-509-494
; Sequence 494, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 494
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-494

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Query Match          31.2%; Score 1280.8; DB 13; Length 1284;
Best Local Similarity 99.8%; Pred. No. 1.6e-308;
Matches 1282; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      485 ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 544
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1   ATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT 60

Qy      545 GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTT 604
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  GATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTT 120

Qy      605 CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTACCC 664

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Db	121	 CGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	180
Qy	665	AGCAATGGCTCAATGCACAACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	724
Db	181	 AGCAATGGCTCAATGCACAACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAA	240
Qy	725	TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGCAACT	784
Db	241	 TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGCAACT	300
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	301	 CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	360
Qy	845	AGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	361	 AGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	420
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	421	 CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	480
Qy	965	TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	481	 TTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	540
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	1084
Db	541	 GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCCTTTG	600
Qy	1085	GTAAGTGGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	601	 GTAAGTGGCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	660
Qy	1145	GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	661	 GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	720
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	721	 CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	780
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	1324
Db	781	 GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGT	840
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	841	 GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	900
Qy	1385	CGTCGAGAAGTGGCAAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTGCTCTTTGCTGGTTC	1444
Db	901	 CGTCGAGAAGTGAAAAAACAGTTTTCTGCTTGGTTGTAATTTTCTGCTCTTTGCTGGTTC	960
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGA	1504

Db 961 CCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAACCGA 1020

Qy 1505 TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG 1564
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1021 TGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG 1080

Qy 1565 AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC 1624
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1081 AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC 1140

Qy 1625 CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG 1684
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1141 CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG 1200

Qy 1685 AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC 1744
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1201 AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC 1260

Qy 1745 AGCCATAAGGACAGCATGAACTGA 1768
 ||||||||||||||||||

Db 1261 AGCCATAAGGACAGCATGAACTGA 1284

RESULT 8

US-10-101-510-59

; Sequence 59, Application US/10101510
 ; Publication No. US20030148295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WAN, JACKSON
 ; APPLICANT: WANG, YIXIN
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 ; FILE REFERENCE: 15117.0012
 ; CURRENT APPLICATION NUMBER: US/10/101,510
 ; CURRENT FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: 60/276,947
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 805
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 59
 ; LENGTH: 560
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-101-510-59

Query Match 12.7%; Score 521; DB 13; Length 560;
 Best Local Similarity 97.7%; Pred. No. 3.4e-119;
 Matches 550; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

Qy 2464 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG 2523
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG 60

Qy 2524 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC 2583
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC 120

Qy 2584 AATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA 2643

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      |||
Db      121 AATCAGATAGTTCTTTTTCACAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA 179
      |||
Qy      2644 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA 2703
      |||
Db      180 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA 239
      |||
Qy      2704 GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG 2763
      |||
Db      240 GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG 299
      |||
Qy      2764 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC 2823
      |||
Db      300 ATTCAGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC 359
      |||
Qy      2824 CTCCTATTCTCTTAATTTTTTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC 2883
      |||
Db      360 CTCCTATTCTCTTAATTTTTTGTTAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTC 419
      |||
Qy      2884 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAA 2943
      |||
Db      420 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAA 479
      |||
Qy      2944 AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA 3003
      |||
Db      480 AAATTAATACCCACAAATGGCACCAG--AACTTACGATTCTTCACTTCTTGGGGTTTTCA 537
      |||
Qy      3004 GTATGAACCTAACTCCCCACCCC 3026
      |||
Db      538 GTATGAACCTAACTCCCCACCCC 560

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RESULT 9

US-09-918-995-8960

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; Sequence 8960, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8960
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(451)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8960

```

Query Match 10.0%; Score 412.4; DB 11; Length 451;
 Best Local Similarity 98.6%; Pred. No. 3.6e-92;
 Matches 416; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy      3347 AGTCCATTTTAACTGTAGCAACCTTCTGCATTATAAATCTTGTAAATCATGTTACCATT 3406
          | | |||||
Db      29  AATTCATTTTAACTGTAGCAACCTTTTGCATTATAAATCTTGTAAATCATGTTACCATT 88

Qy      3407 ACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGT 3466
          |||||
Db      89  ACAAATGGTATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGT 148

Qy      3467 TTTGTTTGGTTGGTTGGTTTGTATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGG 3526
          |||||
Db      149 TTTGTTTGGTTGGTTGGTTTGTATAAAACAGTATTTGGGGTCATATTGATTTCCTGTGCTGG 208

Qy      3527 AGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGA 3586
          |||||
Db      209 AGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGA 268

Qy      3587 TGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATA 3646
          |||||
Db      269 TGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATA 328

Qy      3647 AATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCC 3706
          |||||
Db      329 AATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCC 388

Qy      3707 AGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTA 3766
          |||||
Db      389 AGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTA 448

Qy      3767 TT 3768
          ||
Db      449 TT 450
  
```

RESULT 10

US-10-007-926A-177

; Sequence 177, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007,926A

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 60/254,090

; PRIOR FILING DATE: 2000-12-08

; NUMBER OF SEQ ID NOS: 468

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 177
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: endothelin receptor type b (EDNRB) gene.
US-10-007-926A-177

Query Match 9.6%; Score 395.8; DB 13; Length 4286;
Best Local Similarity 65.7%; Pred. No. 2.6e-87;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

```
Qy      689 TGCCACAGCAGACTAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy      749 ACTATTTTTCATCGTGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
      | | ||| | | | | | | | | | | | | | | | | | | | | | |
Db      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
      || | | ||| | | | | | | | | | | | | | | | | | | | |
Db      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGCAGAAGTCCTCG 988
      ||||| | | | | | | | | | | | | | | | | | | | | |
Db      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789

Qy      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048
      ||||| ||||| | | | | | | | | | | | | | | | | | | |
Db      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849

Qy      1049 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909

Qy      1109 ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTTCATGGTACCC 1168
      || | | | | | | | | | | | | | | | | | | | | | | |
Db      910 ATTTGGGTGGTCTCTGTGGTTCGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969

Qy      1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT 1029

Qy      1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282
      ||||| ||||| ||| | | | | | | | | | | | | | | | | |
Db      1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG 1089

Qy      1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342
      || |||| | | | | | | | | | | | | | | | | | | | |
Db      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146

Qy      1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402
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Db	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Db	1207	ACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG	1266
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGTAGCTTT	1326
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1327	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1386
Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1387	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC	1446
Qy	1643	TGCTG	1647
Db	1447	TGGTG	1451

US-09-921-406C-13

; Sequence 13, Application US/09921406C

; GENERAL INFORMATION:

; APPLICANT: Yakhini, Zohar

; APPLICANT: Ben-Dor, Ami

; APPLICANT: Sampas, Nick

; APPLICANT: Dougherty, Edward

; APPLICANT: Trent, Jeff

; APPLICANT: Meltzer, Paul

; APPLICANT: Chen, Yidong

; APPLICANT: Weeraratna, Ashani

; APPLICANT: Jiang, Yuan

; APPLICANT: Bittner, Michael

```
; TITLE OF INVENTION: Classifying Cancers
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; FILE REFERENCE: 10010313-1

; CURRENT APPLICATION NUMBER: US/09/921,406C

; CURRENT FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 41

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; SOFTWARE: PatentIn Ver. 2.1

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SEQ ID NO 13

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 9.6%; Score 395.8; DB 13; Length 4286;

Best Local Similarity 65.7%; Pred. No. 2.6e-87;

Qy 689 TGCCCAAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy 689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Db 505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy 749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy 809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy 869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740

Qy 929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAGAAGTCCTCG 988
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 741 -----ATTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 789

Qy 989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC 1048
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849

Qy 1049 TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108
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Db 850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909

Qy 1109 ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC 1168
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Db 910 ATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969

Qy 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
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Db 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029

Qy 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1030 TTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTG 1089

Qy 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG--AGAAAG 1146

Qy 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402
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Db 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206

Qy 1403 ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462
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Db 1207 ACCGTCTTTTGCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACTCAGCAGG 1266

Qy 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522
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Db 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTGAGCTTT 1326

Qy 1523 TTAAGTCTCATGGATTACATCGGTATTAACCTTGGCAACCATGAATTCATGTATAAACCCC 1582
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Db 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386


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Qy      1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642
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Db      1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446

Qy      1643 TGCTG 1647
          || ||
Db      1447 TGGTG 1451

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RESULT 12

US-10-210-120-15

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; Sequence 15, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-15

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Query Match          9.6%; Score 395.8; DB 13; Length 4286;
Best Local Similarity 65.7%; Pred. No. 2.6e-87;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
          ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
          | | ||| | |||| | | |||| | | | | | | | | | | | | | |
Db      565 CTTGTGTTCTGTCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868
          || || ||| | || | |||| | |||| | ||| | | | | | | | |
Db      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
          | | ||||| | ||||| ||||| | ||||| ||||| | | |||||
Db      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----- 740

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCCTTTTTCAGAGAAGTCCTCG 988
          ||||| | | | ||||| | | | | | | | | | | | | | |
Db      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789

```



```

; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-113

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Query Match          9.6%; Score 395.8; DB 15; Length 4286;
Best Local Similarity 65.7%; Pred. No. 2.6e-87;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748
      |||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564

Qy      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC 808
      |  |  |||  |  ||||  |  |  ||||  |  |  |||  |  |  |||  |  |  |||  |
Db      565 CTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624

Qy      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868
      ||  ||  |||  |  ||  |||  |  ||  ||||  |  ||  |||  |  ||  |||  |  |
Db      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684

Qy      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
      |  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740

Qy      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTGAGAGTCTCTCG 988
      |||||  |  |  ||  |||||  |  ||  ||  |  |||||  |  |||||  |  |||||
Db      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTATACAGAAAGCCTCC 789

Qy      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC 1048
      |||||  |||||  |  ||  |  ||  |  |||||  |  |||||  |  |||||  |  |||||
Db      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849

Qy      1049 TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1108
      ||  |||||  |  ||  |||||  |  |||||  |  ||  ||  |  |||||  |  |||||
Db      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909

Qy      1109 ATCTGGATCCTGTCTTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC 1168
      ||  |||  |  |  |  |  ||||  |  ||||  |  ||||  |  ||||  |  ||||  |
Db      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969

Qy      1169 TTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
      |  ||  ||  |  ||  |  ||  ||||  |  ||||  |  ||||  |  ||||  |  ||||
Db      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT 1029

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Qy 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282
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 Db 1030 TTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTCAATTTCTATTTCTGCTTG 1089

Qy 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342
 || |||| | |||| | || | | | |||| | |||| | |||| | |||| |
 Db 1090 CCATTGGCCATCACTGCATTTTTTTATACATAATGACCTGTGAAATGTTG--AGAAAG 1146

Qy 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402
 || | || | | |||| | | || | | | |||| | | ||||| ||||| ||
 Db 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206

Qy 1403 ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462
 || || | || | |||| | | |||| | | |||| | | |||| | |||| |
 Db 1207 ACCGTCTTTGCTTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACTCAGCAGG 1266

Qy 1463 ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522
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 Db 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGTAGCTTT 1326

Qy 1523 TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582
 | || | |||| | | |||| | || |||| | | ||||| ||| | ||||| ||
 Db 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386

Qy 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642
 || ||||| ||||| ||||| | ||| |||| | || | ||||| ||| ||||| ||
 Db 1387 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAACTGCTTTAAGTCATGCTTATGCTGC 1446

Qy 1643 TGCTG 1647
 || ||
 Db 1447 TGGTG 1451

RESULT 14

US-09-931-157-2

; Sequence 2, Application US/09931157
 ; Patent No. US20020082414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Imura, Hiroo
 ; APPLICANT: Nakao, Kazuwa
 ; APPLICANT: Nakanishi, Shigetada
 ; TITLE OF INVENTION: Human Endothelin Receptor
 ; FILE REFERENCE: 299002032411
 ; CURRENT APPLICATION NUMBER: US/09/931,157
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 08/121,446
 ; PRIOR FILING DATE: 1993-09-14
 ; PRIOR APPLICATION NUMBER: 07/911,684
 ; PRIOR FILING DATE: 1992-07-10
 ; PRIOR APPLICATION NUMBER: JP 3-172828
 ; PRIOR FILING DATE: 1991-07-12
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 4301
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)...(1566)
US-09-931-157-2

Query Match 9.6%; Score 395.8; DB 9; Length 4301;
Best Local Similarity 65.7%; Pred. No. 2.6e-87;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

Qy	689	TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT	748
Db	505	TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC	564
Qy	749	ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC	808
Db	565	CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC	624
Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC	868
Db	625	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	684
Qy	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Qy	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTTGCAGAAGTCCTCG	988
Db	741	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	789
Qy	989	GTGGGGATCACCCTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Qy	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Db	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Qy	1109	ATCTGGATCCTGTCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTCATGGTACCC	1168
Db	910	ATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	1029
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Db	1030	TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG	1089
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG	1146
Qy	1343	AATGGCAGCTTGAGAAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206

Qy 1403 ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462
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 Db 1207 ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG 1266

Qy 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522
 || || || || || || || || || || || || || || || || || || || || ||
 Db 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGTAGCTTT 1326

Qy 1523 TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582
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 Db 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386

Qy 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642
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 Db 1387 ATTGCTCTGTATTTGGTGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446

Qy 1643 TGCTG 1647
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 Db 1447 TGGTG 1451

RESULT 15

US-09-826-509-496

; Sequence 496, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 496

; LENGTH: 1329

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-826-509-496

Query Match 9.6%; Score 392.6; DB 13; Length 1329;

Best Local Similarity 65.5%; Pred. No. 6.9e-87;

Matches 632; Conservative 0; Mismatches 309; Indels 24; Gaps 3;

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 Db 268 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 327

Qy 749 ACTATTTTCATCGTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808
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Db	328	CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC	387
Qy	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC	868
Db	388	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	447
Qy	869	TATGTGGTCAATTGATCTCCCTATCAAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Db	448	CACATCGTCATTTGACATCCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	503
Qy	929	GATCACAATGACTTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAGAAGTCCTCG	988
Db	504	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	552
Qy	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Db	553	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	612
Qy	1049	TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
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Qy	1109	ATCTGGATCCTGTCTTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTTCATGGTACCC	1168
Db	673	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTGTATATAATTACG	732
Qy	1169	TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Db	733	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT	792
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Qy	1403	ACAGTTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT	1462
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Qy 1643 TGCTG 1647
|| ||
Db 1210 TGGTG 1214

Search completed: December 13, 2003, 00:41:34
Job time : 1215.3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:56 ; Search time 949.825 Seconds
(without alignments)
11666.569 Million cell updates/sec

Title: US-09-931-157-1
Perfect score: 4105
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	4105	100.0	4105	24	ABZ35259		Human gene express
2	4105	100.0	4105	24	ABV94238		Breast carcinoma r
3	4105	100.0	4105	25	ABZ42662		Human endothelin A
4	4103.4	100.0	4105	14	AAQ34583		ETa receptor gene.
5	4103	100.0	4105	21	AAA38341		Human endothelin r
6	4079	99.4	4079	25	ACA56659		Human signalling p
7	2470	60.2	2595	24	AAL39858		Human allergy-asso
8	2470	60.2	2595	24	ABK94408		DNA encoding endot
9	2470	60.2	2595	24	ABK35492		Human endometrial
10	1819.6	44.3	1868	21	AAF20903		Human low adenosin
11	1819.6	44.3	1868	21	AAF20915		Human endothelin r
12	1819.6	44.3	1868	21	AAA34781		Human adenosine re
13	1819.6	44.3	1868	21	AAA34793		Human adenosine re
14	1819.6	44.3	2008	21	AAF20904		Human low adenosin
15	1819.6	44.3	2008	21	AAA34782		Human adenosine re
16	1819.6	44.3	5036	21	AAF21447		Human endothelin r
17	1819.6	44.3	117609	21	AAF21435		Human receptor-rel
18	1296.8	31.6	1310	21	AAF20902		Human endothelin r
19	1296.8	31.6	1310	21	AAF20914		Human ELAM-1 polyn
20	1296.8	31.6	1310	21	AAA34780		Human adenosine re
21	1296.8	31.6	1310	21	AAA34792		Human adenosine re
22	1296.8	31.6	146981	21	AAF21442		Human ELAM-1 polyn
23	1280.8	31.2	1284	23	ABI97987		Non-endogenous hum
24	1248.8	30.4	1284	15	AAQ63209		Human endothelin r
25	521	12.7	560	24	ABZ34947		Human gene express
26	403.8	9.8	1965	13	AAQ25892		Sequence encodes e
27	399	9.7	4301	14	AAQ34584		ETb receptor gene.
28	396.6	9.7	1406	15	AAQ53922		Bovine ET receptor
29	395.8	9.6	1470	25	ACA56605		Human signalling p
30	395.8	9.6	1632	24	AAD24966		Human G-protein co
31	395.8	9.6	1719	21	AAF21285		Human low adenosin
32	395.8	9.6	1720	21	AAA35163		Human adenosine re
33	395.8	9.6	1872	21	AAF21283		Human low adenosin
34	395.8	9.6	1872	21	AAA35161		Human adenosine re
35	395.8	9.6	1873	19	AAV17875		Homo sapiens endot
36	395.8	9.6	4286	21	AAF21284		Human low adenosin
37	395.8	9.6	4286	21	AAA35162		Human adenosine re
38	395.8	9.6	4286	24	ABV94186		Breast carcinoma r
39	395.8	9.6	4286	25	ABZ42661		Human endothelin B
40	395.8	9.6	13611	21	AAF21288		Human low adenosin
41	395.8	9.6	13612	21	AAA35166		Human adenosine re
42	392.6	9.6	1329	23	ABI97988		Non-endogenous hum
43	383.2	9.3	1958	24	ABI99321		Mouse ischaemic co
44	381.2	9.3	1578	21	AAF21287		Human low adenosin
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ALIGNMENTS

RESULT 1

ABZ35259

ID ABZ35259 standard; cDNA; 4105 BP.

XX

AC ABZ35259;

XX

DT 05-FEB-2003 (first entry)

XX

DE Human gene expression profile polynucleotide SEQ ID NO 370.

XX

KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW gene expression; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200274979-A2.

XX

PD 26-SEP-2002.

XX

PF 20-MAR-2002; 2002WO-US08456.

XX

PR 20-MAR-2001; 2001US-276947P.

XX

PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX

PI Wan J, Wang Y;

XX

DR WPI; 2002-740862/80.

XX

PT New gene expression profile generated from primary, endothelial,
PT epithelial, and muscle cell types, useful for identifying disease
PT pathologies involving alterations of gene expression, e.g. cancer -

XX

PS Disclosure; Page 513-515; 850pp; English.

XX

CC The invention relates to a gene expression profile comprising one or more
CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC is a coronary artery endothelium, umbilical artery or vein endothelium,
CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC endothelium, myometrium microvascular endothelium, keratinocyte
CC epithelium, bronchial epithelium, mammary epithelium, prostate
CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC small airway epithelium, renal epithelium, umbilical artery smooth
CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC osteoblasts or prostate stromal cell. The gene expression profile is used
CC for determining the level of RNA expression for a sample, determining the
CC phenotype of a cell and distinguishing cell types. The gene or a protein
CC expression profile is useful in identifying disease pathologies
CC involving alterations of gene expression. The assessment of expression
CC profiles may provide meaningful information with respect to tumour type
CC and stage, treatment methods, and prognosis. The gene or protein

CC expression profile may also be used for creating microarrays. The
CC microarray is useful for genetic and physical mapping of genomes, DNA
CC sequencing, genetic or medical diagnosis, genotyping of organisms,
CC confirming cell or tissue identifications and in identifying promising
CC antibiotics, antiviral or antifungal agents.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 other;

Query Match 100.0%; Score 4105; DB 24; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
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Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
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Qy    661 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720
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Db	721	CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
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Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
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Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
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Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
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Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
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Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
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Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCCACCATTTCAAAG	3060
Qy	3061	GGCCCAAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Qy 3241 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA 3300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3241 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA 3300

Qy 3301 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC 3360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3301 GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC 3360

Qy 3361 TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA 3420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3361 TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA 3420

Qy 3421 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT 3480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3421 AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT 3480

Qy 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA 3540

Qy 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3541 CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT 3600

Qy 3601 TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3601 TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA 3660

Qy 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3661 ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG 3720

Qy 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3721 CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG 3780

Qy 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3781 CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG 3840

Qy 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900

Qy 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960

Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020

Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

Db 4081 TAAATATAAGTTTACAGAACCTT 4105

RESULT 2

ABV94238

ID ABV94238 standard; cDNA; 4105 BP.

XX

AC ABV94238;

XX

DT 08-JAN-2003 (first entry)

XX

DE Breast carcinoma related nucleotide sequence SEQ ID NO:229.

XX

KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour;
KW gene; ss.

XX

OS Homo sapiens.

XX

PN WO200246467-A2.

XX

PD 13-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-IB02811.

XX

PR 08-DEC-2000; 2000US-254090P.

PR 07-DEC-2001; 2001US-0007926.

XX

PA (IPSO-) IPSOGEN.

XX

PI Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;

XX

DR WPI; 2002-619023/66.

XX

PT Novel polynucleotide library useful in molecular characterization of a
PT carcinoma, comprising a pool of polynucleotide sequences or its
PT subsequences which are either underexpressed or overexpressed in tumor
PT cells -

XX

PS Claim 1; Page 258-259; 401pp; English.

XX

CC The present invention describes a polynucleotide library (I) useful in
CC the molecular characterisation of a carcinoma, comprising a pool of
CC polynucleotides or its subsequences which are either underexpressed or
CC overexpressed in tumour cells, and correspond to any of the
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
CC (M1) differentially expressed polynucleotide sequences which are
CC correlated with a cancer, involves obtaining a polynucleotide sample from
CC a patient, and reacting the polynucleotide sample obtained with a probe
CC immobilised on a solid support, where the probe comprises any combination
CC of the polynucleotide sequences of (I) or its expression products encoded
CC by polynucleotide sequences of (I), and detecting the reaction product.
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
CC useful for the prognosis or diagnostic of tumour, in differentiating a

CC normal cell from a cancer cell, detecting a hormone sensitive tumour
CC cell, differentiating a tumour with lymph nodes from a tumour without
CC lymph nodes, differentiating antracycline-sensitive tumours from
CC antracycline-insensitive tumours, and classifying good and poor prognosis
CC primary breast tumours. (I) is useful for large-scale molecular
CC characterisation of breast cancer that help in prediction, prognosis and
CC cancer treatment, and for detecting differentially expressed genes that
CC correlated with a cancer.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 other;

Query Match 100.0%; Score 4105; DB 24; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60
      |||
Db      1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCGTGCGAGCCCT 120
      |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCGTGCGAGCCCT 120

Qy    121 CGCGCGCGGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||
Db    121 CGCGCGCGGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||
Db    181 CATCCATCCCACCCGGTCGTGCGCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
      |||
Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
      |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
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Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500

Qy	1501	CCGATGTGAATTACTTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Db	1681	CATGAACGGAAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAAC TGACCACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAAC TGACCACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATT CAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATT CAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCCCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCAC TTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCAC TTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340

Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAAAATTTTCATTTCAGGTATTTTGTAAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAAATTTTCATTTCAGGTATTTTGTAAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGTCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Db	3181		ATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241		GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241		GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301		GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301		GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361		TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361		TGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421		AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421		AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481		TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481		TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541		CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541		CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601		TGTCTGATATTTCTTTTCACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601		TGTCTGATATTTCTTTTCACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661		ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661		ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721		CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721		CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781		CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781		CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841		ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841		ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901		ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901		ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961		TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961		TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021		AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTG	4080

Db 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080

Qy 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

Db 4081 TAAAATAAAAGTTTACAGAAACCTT 4105

RESULT 3

ABZ42662

ID ABZ42662 standard; DNA; 4105 BP.

XX

AC ABZ42662;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human endothelin A receptor nucleotide SEQ ID NO:115.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US50107.

XX

PR 19-DEC-2000; 2000US-257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR

P-PSDB; ABP81816.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 845 G; 1263 T; 0 other;

Query Match 100.0%; Score 4105; DB 25; Length 4105;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG	60
Db	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGAAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCA GTGCC CAGGAAGTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCA GTGCC CAGGAAGTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480

Db	421	 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320

Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTGTATTAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTGTATTAGCACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACGGTCACCATGAACTTTAG	2160

Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Db	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000

Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA	3060
Qy	3061	GGCCCAAGTGAAGTTTGGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGAAGTTTGGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACCTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTGTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTACACCATTTTGTGTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900

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      |||
Db      3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
Qy      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
      |||
Db      3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
Qy      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
      |||
Db      3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
Qy      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
      |||
Db      4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
Qy      4081 TAAAATAAAAGTTTACAGAAACCTT 4105
      |||
Db      4081 TAAAATAAAAGTTTACAGAAACCTT 4105

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RESULT 4

AAQ34583

ID AAQ34583 standard; DNA; 4105 BP.

XX

AC AAQ34583;

XX

DT 25-MAR-2003 (updated)

DT 11-MAY-1993 (first entry)

XX

DE ETa receptor gene.

XX

KW Human; ETa; ETb; endothelin; receptor; transmembrane domain; N tail;

KW extracellular; cytoplasmic; C tail; post translational; bovine;

KW modification; ET-1 receptor; antagonist; circulatory system; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	CDS	485..1768
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FT		/*tag= a
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FT	sig_peptide	485..544
----	-------------	----------

FT		/*tag= b
----	--	----------

FT	mat_peptide	545..1765
----	-------------	-----------

FT		/*tag= c
----	--	----------

FT	polyA_signal	4084..4089
----	--------------	------------

FT		/*tag= d
----	--	----------

FT	misc_feature	1972..1976
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FT		/*tag= e
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FT		/function= Related with mRNA instability
----	--	--

FT	misc_feature	2059..2063
----	--------------	------------

FT		/*tag= f
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FT		/function= Related with mRNA instability
----	--	--

FT	misc_feature	2309..2313
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FT		/*tag= g
----	--	----------

FT		/function= Related with mRNA instability
----	--	--

FT	misc_feature	2386..2390
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FT		/*tag= h
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FT          /function= Related with mRNA instability
FT  misc_feature  2680..2684
FT          /*tag= i
FT          /function= Related with mRNA instability
FT  misc_feature  3252..3256
FT          /*tag= j
FT          /function= Related with mRNA instability
FT  misc_feature  3944..3948
FT          /*tag= k
FT          /function= Related with mRNA instability
XX
PN  EP522868-A1.
XX
PD  13-JAN-1993.
XX
PF  10-JUL-1992;  92EP-0306347.
XX
PR  12-JUL-1991;  91JP-0172828.
XX
PA  (SHIO ) SHIONOGI SEIYAKU KK.
XX
PI  Imura H,  Nakanishi S,  Nakao K;
XX
DR  WPI; 1993-010677/02.
DR  P-PSDB; AAR30885.
XX
PT  Human ETa and ETb endothelin receptors - for measuring endothelin
PT  and screening for endothelin antagonists
XX
PS  Claim 6; Fig 1; 39pp; English.
XX
CC  The sequences given in AAQ34583-84 encode the human ETa and ETb
CC  endothelin receptors respectively.  ETa is a 427 amino acid protein
CC  with a molecular weight of 48,726.  ETb comprises 442 amino acids and
CC  has a molecular weight of 49,629.  ETa has a higher affinity for
CC  endothelin (ET)-1 and ET-2, whereas ETb has no selectivity for ET-1,
CC  ET-2 or ET-3.  The receptors each contain seven transmembrane domains
CC  and have an extracellular N tail and a cytoplasmic C tail.  There are
CC  several potential sites for post translational modification, these
CC  sites are identical to those of bovine ET-1 receptor.  ETa cDNA is
CC  91.2% homologous to bovine ET-1 receptor cDNA and ETb cDNA is 61.1%
CC  homologous to that of bovine ETa-receptor.  The receptor proteins are
CC  useful as reagents for measuring the amount of ET or screening for
CC  antagonists of the ET receptor when studying the circulatory system.
CC  (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ  Sequence 4105 BP; 1138 A; 860 C; 844 G; 1263 T; 0 other;

Query Match          100.0%;  Score 4103.4;  DB 14;  Length 4105;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 4104;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy          1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60
          |||
Db          1 GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy          61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGAGTTTTCTTTTCGTGCGAGCCCT 120

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Db	61	 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTCGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACCATTTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	 CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	 AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960

Db	901	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTTGAGAAAGTCCTCGGTGGGGATCACCGTCTCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAAGTCCTCGGTGGGGATCACCGTCTCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAAACAGCATCCAGTGGAAGAACACGATCAAAACAACCAACACAGACCG	1740
Db	1681	CATGAACGGAAACAGCATCCAGTGGAAGAACACGATCAAAACAACCAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800

Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640

Qy	2641	AAAAATCAATGTCAAGTACCAAAATGTTAAATGTATGTGTGTCATTTAACTCTGCCTGAGACTTT	2700
Db	2641	AAAAATCAATGTCAAGTACCAAAATGTTAAATGTATGTGTGTCATTTAACTCTGCCTGAGACTTT	2700
Qy	2701	TCAGTGCACCTGTATATAGAAAGTCTAAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACCTGTATATAGAAAGTCTAAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTTCGGAAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTGTTAAATGTTAACTGGCAGTAAGTCTTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACCTCTTGGGGTTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCCAAGTGAAGTCTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCCAAGTGAAGTCTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGTATAAAGCAGTATTTGGGGTTCATATTGTTTCTGTGCTGGAGCAAAAGTCATTA	3540

Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

RESULT 5

AAA38341

ID AAA38341 standard; DNA; 4105 BP.

XX

AC AAA38341;

XX

DT 21-AUG-2000 (first entry)

XX

DE Human endothelin receptor type A gene coding region.

XX

KW Endothelin receptor type A gene; coding region;

KW polymorphism; polymorphic marker; cardiovascular disease;

KW myocardial infarction; unstable angina; hypertension; atherosclerosis;

KW stroke; prognosis; drug screening; treatment outcome; human; ds.
XX
OS Homo sapiens.
XX
PN WO200022166-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB01678.
XX
PR 14-OCT-1998; 98US-0104286.
PR 14-OCT-1998; 98US-0104302.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
DR WPI; 2000-318010/27.
XX
PT Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern -
XX
PS Disclosure; Page 125-126; 126pp; English.
XX
CC The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to
CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be
CC non-responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby

CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. The present
CC sequence represents the human endothelin receptor type A gene
CC coding region (GenBank S57498). The polymorphic sites identified are
CC 969C/T, 1005A/G, 1146A/G and 2485T/C.

XX

SQ Sequence 4105 BP; 1138 A; 859 C; 843 G; 1263 T; 2 other;

Query Match 100.0%; Score 4103; DB 21; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60
      |||
Db      1 GAATTCGCGGCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGCGAGCCCT 120
      |||
Db     61 AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCGGAGTTTTCTTTTTCTGCGAGCCCT 120

Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
      |||
Db    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
      |||
Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300
      |||
Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
      |||
Db    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360

Qy    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420
      |||
Db    361 TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA 420

Qy    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480
      |||
Db    421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
      |||
Db    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Qy    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600
      |||
Db    541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC 600

Qy    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660
      |||
Db    601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660

Qy    661 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720
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Db	661	 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCCTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTCAATGGTACCCCTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTCAATGGTACCCCTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAANNAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560

Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTFTTAAGTGATTTTTTGTCTTCAGCCAAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTFTTAAGTGATTTTTTGTCTTCAGCCAAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAA	2400

Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240

Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAAATTGTGCCCCGCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG	4080
Db	4021	AGTAACTTTGTAGAAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAAGTG	4080
Qy	4081	TAAAAATAAAAGTTTACAGAAACCTT	4105

|||||
Db 4081 TAAATAAAAGTTTACAGAACCTT 4105

RESULT 6

ACA56659

ID ACA56659 standard; cDNA; 4079 BP.

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AC ACA56659;

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DT 06-JUN-2003 (first entry)

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DE Human signalling pathway polynucleotide probe SEQ ID NO 1257.

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KW Human; probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

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OS Homo sapiens.

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PN US6500938-B1.

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PD 31-DEC-2002.

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PF 30-JAN-1998; 98US-0016434.

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PR 30-JAN-1998; 98US-0016434.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Au-Young J, Seilhamer JJ;

XX

DR WPI; 2003-352189/33.

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PT Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

PT polynucleotides -

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PS Claim 1; SEQ ID NO 1257; 65pp; English.

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CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease

Db	661	 AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAA	720
Qy	725	TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGCAACT	784
Db	721	 TACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	 CTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGGCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	 AGTCTTGGCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	 CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	 TTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020
Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCCCTTG	1084
Db	1021	 GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCCCTTG	1080
Qy	1085	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	1081	 GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1204
Db	1141	 GCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	 CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACCTCGATCTTCTACACCTCATGACTTGT	1324
Db	1261	 GGGTTCTATTTCTGTATGCCCTTGGTGTGCACCTCGATCTTCTACACCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	 GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1444
Db	1381	 CGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	 CCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTCCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATG	1564

Db	1501	TGTGAATTACTTAGTCTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATC	1800
Qy	1805	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924
Db	1861	TTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
Qy	1925	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1984
Db	1921	TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAGAGAT	2164
Db	2101	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACCTGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	GGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2344
Db	2281	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAATA	2340
Qy	2345	GTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTAAACAC	2404
Db	2341	GTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACCTATTTATTTTTTTAAACAC	2400

Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
Db	2461	GCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2520
Qy	2525	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCA	2584
Db	2521	TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCA	2580
Qy	2585	ATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2644
Db	2581	ATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAAA	2640
Qy	2645	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCAG	2704
Db	2641	TCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCAG	2700
Qy	2705	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2764
Db	2701	TGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATGA	2760
Qy	2765	TTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2824
Db	2761	TTCGGAAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATATCACC	2820
Qy	2825	TCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2884
Db	2821	TCCTATTCTCTTAATTTTTGTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCC	2880
Qy	2885	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2944
Db	2881	CTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAA	2940
Qy	2945	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3004
Db	2941	AATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTTCAG	3000
Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3064
Db	3001	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3060
Qy	3065	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3124
Db	3061	CACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAA	3120
Qy	3125	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATTT	3184
Db	3121	TCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATTT	3180
Qy	3185	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3244
Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240

Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
Db	3301	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3360
Qy	3365	GCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600
Qy	3605	TGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3664
Db	3601	TGATATTTCTTTCAGACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTT	3660
Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
Db	3781	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3840
Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3904
Db	3841	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTC	3900
Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964
Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4020
Qy	4025	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4083
Db	4021	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTA	4079

RESULT 7

AAL39858

ID AAL39858 standard; DNA; 2595 BP.

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AC AAL39858;

XX

DT 05-SEP-2002 (first entry)

XX

DE Human allergy-associated gene SEQ ID No 30.

XX

KW Antiallergic; allergic disease; carboxypeptidase M; cathepsin C; CYP1B1;
KW endoserine A receptor; osteoblast-specific factor 2; DD96; gene therapy;
KW bronchial asthma; human; ds.

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OS Homo sapiens.

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PN WO200252006-A1.

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PD 04-JUL-2002.

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PF 21-DEC-2001; 2001WO-JP11287.

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PR 26-DEC-2000; 2000JP-0396166.

XX

PA (GENO-) GENOX RES INC.

XX

PI Ohtani N, Matsui K, Yoshida N, Sugita Y, Izuhara K;

XX

DR WPI; 2002-500763/53.

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PT Examining allergic diseases by changes in expression levels of six
PT allergy-associated genes inducible by stimulation e.g. of airway
PT epithelia cells with interleukin-4 or 13, also applicable in screening
PT compounds -

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PS Disclosure; Page 79-80; 106pp; Japanese.

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CC The invention relates to a novel method for examining allergic diseases,
CC comprising determining the expression level of a gene selected from
CC carboxypeptidase M, cathepsin C, endoserine A receptor, osteoblast-
CC specific factor 2, DD96 and CYP1B1 in the biological sample from a
CC patient, and comparing the expression level with that in the sample of a
CC healthy individual. The polynucleotides of the invention can be used to
CC treat disorders by gene therapy. The method is useful for examining
CC allergic diseases particularly bronchial asthma and its diagnosis, which
CC is also applicable in screening candidate compounds for remedies. This
CC polynucleotide sequence represents a human allergy-associated gene of the
CC invention.

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SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;

Query Match 60.2%; Score 2470; DB 24; Length 2595;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1624 CCAGTCATGCCTCTGCTGCTGCTGTTACCAAGTCTGATGACCTCGGTCCCAT 1683
|||||

Db	15	CCAGTCATGCCTCTGCTGCTGCTTTACCAAGTCCAAAAAGTCTGATGACCTCGGTCCCCAT	74
Qy	1684	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCACAACACAGACCGGAG	1743
Db	75	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAAACAACCACAACACAGACCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	1863
Db	195	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	254
Qy	1864	CTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGACTG	1923
Db	255	CTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGACTG	314
Qy	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGTTAAA	2043
Db	375	TGCGTGTGTATTTCAGCACTAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAAACA	794
Qy	2404	CAAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAATTCCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914

Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGATG	1153
Qy	2764	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGCCAGATGAGTTTATCATGTCAAGTAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGCCAGATGAGTTTATCATGTCAAGTAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACTGT	1753

Qy	3364	AGCAACCTTCTGCATTTCATAAATCTTGTAAATCATGTTACCATTTACAAATGGGATATAAGA	3423
Db	1754		
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTTGGTTGGTTGG	3483
Db	1814		
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874		
Qy	3544	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3603
Db	1934		
Qy	3604	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3663
Db	1994		
Qy	3664	CTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAAATTAGGTAAGATAATT	3723
Db	2054		
Qy	3724	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3783
Db	2114		
Qy	3784	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3843
Db	2174		
Qy	3844	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3903
Db	2234		
Qy	3904	ATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	3963
Db	2294		
Qy	3964	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	4023
Db	2354		
Qy	4024	CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT	4083
Db	2414		
Qy	4084	AATTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGGTGTA	4105
Db	2474		
Qy	4105	AATTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGGTGTA	4164
Db	2495		

RESULT 8

AC ABK94408;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE DNA encoding endothelin receptor A (EDNRA), exon 8.
 XX
 KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRA;
 KW endothelin receptor A; signaling system; cardiovascular disease;
 KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;
 KW fatty acid metabolism; diabetes; familial hypercholesterolaemia;
 KW forensic marker; transgenic animal; solid support; SNP;
 KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(1830,G)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism"
 XX
 PN WO200224747-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-EP10087.
 XX
 PR 19-SEP-2000; 2000EP-0120123.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Brinkmann U, Hoffmeyer S;
 XX
 DR WPI; 2002-435060/46.
 XX
 PT Novel polynucleotide of the endothelin/endothelin converting
 PT enzyme/receptors of endothelin and endothelin converting enzyme
 PT signaling system associated with cardiovascular disease, useful for
 PT treating the disease -
 XX
 PS Claim 1; Page -; 190pp; English.
 XX
 CC The invention describes a polynucleotide (I) of the endothelin
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 CC signaling system which is associated with a cardiovascular disease. (I),
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
 CC or (II) is useful for producing cells capable of expressing a molecular
 CC variant polypeptide which is associated with a cardiovascular disease.
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
 CC a molecular variant gene comprising (I) is useful for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
 CC or its gene product, or for identifying and obtaining an inhibitor of
 CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
 CC signaling system or its gene product. The isolated proteins and
 CC polynucleotides encoding them are useful for preparation of a
 CC pharmaceutical composition for treating a cardiovascular disease such as
 CC coronary heart disease, hypertension, atherosclerosis, or related to

Db	615	 TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	2343
Db	675	 TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAACA	2403
Db	735	 AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATTTATTTTTTTTAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	 CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	 GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCCTC	2583
Db	915	 GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCCTC	974
Qy	2584	AATCAGATAGTTCTTTTTTCAAGTTCAATACGTTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	 AATCAGATAGTTCTTTTTTCAAGTTCAAT-CTGTTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	 ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	 GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	 ATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTGTAAAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTCT	2883
Db	1214	 CTCCTATTCTCTTAATTTTTGTAAAAATGTAACTGGCAGTAAGTCTTTTTTGATCATTCT	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	2943
Db	1274	 CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	 AAATAATTACCCACAAATGCCACCAGTAACCTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	3063
Db	1394	 GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123

Db	1454	CCACAGTGACTTTTGGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
Db	1874	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	TGTTGGGCCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	2353

Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413

Qy 4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 4083
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 2473

Qy 4084 AATAAAAGTTTACAGAAACCTT 4105
 ||||||||||||||||
 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 9

ABK35492

ID ABK35492 standard; DNA; 2595 BP.

XX

AC ABK35492;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human endometrial cancer related gene, EDNRA.

XX

KW Human; ds; gene; endometrial cancer; differential expression;

KW DNA microarray; protein microarray.

XX

OS Homo sapiens.

XX

PN WO200209573-A2.

XX

PD 07-FEB-2002.

XX

PF 31-JUL-2001; 2001WO-US24104.

XX

PR 31-JUL-2000; 2000US-221735P.

XX

PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

XX

PI Mutter GL;

XX

DR WPI; 2002-179967/23.

DR P-PSDB; AAU84272.

XX

PT Diagnosing endometrial cancer comprises determining expression of
 PT nucleic acid molecules or expression products that are differentially
 PT expressed in normal and malignant endometrium -

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PS Claim 1; Page 60-62; 233pp; English.

XX

CC The invention relates to diagnosing endometrial cancer in a subject
 CC suspected of having endometrial cancer comprising determining the
 CC expression of a set of nucleic acid molecules or expression products in
 CC an endometrial sample suspected of being cancerous, where the set of
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules
 CC selected from 50 fully defined sequences as given in the specification.
 CC The nucleic acids are used as an array of at least 2 of the 50

CC nucleic acids bound to a solid substrate. Also included is a solid-phase
CC protein microarray comprising at least 2 antibodies or its antigen
CC binding fragments, that specifically bind at least 2 different
CC polypeptides from the 50 fully defined sequences as given in the
CC specification, fixed to a solid substrate. The methods and arrays are
CC useful for the diagnosis of endometrial cancer, selecting and monitoring
CC treatment regimes and identification of lead compounds useful for the
CC treatment of endometrial cancer. The present sequence is one of 50
CC genes differentially expressed between cancerous and non-cancerous
CC samples.

XX

SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;

Query Match 60.2%; Score 2470; DB 24; Length 2595;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1624	CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT	1683
Db	15	CCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCAT	74
Qy	1684	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	1743
Db	75	GAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAG	134
Qy	1744	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	1803
Db	135	CAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAT	194
Qy	1804	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	1863
Db	195	CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTT	254
Qy	1864	CTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	1923
Db	255	CTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTG	314
Qy	1924	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	1983
Db	315	GTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTC	374
Qy	1984	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	2043
Db	375	TGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAA	434
Qy	2044	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	2103
Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTA	494
Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGA	2163
Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614

Qy	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAA	674
Qy	2284	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGGAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGGAAAAAAGACAAAAAT	734
Qy	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
Db	915	GTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTTCA	1093
Qy	2704	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	2763
Db	1094	GTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAGATG	1153
Qy	2764	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTTCGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCTATTCTCTTAATTTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	2883
Db	1214	CTCCTATTCTCTTAATTTTTTGTTAAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATTC	1273
Qy	2884	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTTCAGTGAA	2943
Db	1274	CCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTTCAGTGAA	1333
Qy	2944	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	3003
Db	1334	AAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTTTCA	1393
Qy	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAGGGC	3063
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACATTTCAAAGGGC	1453
Qy	3064	CCACAGTGACTTTTGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123

Db	1454	 CCACAGTGACTTTTGGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	3183
Db	1514	 ATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCCATT	1573
Qy	3184	TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	3243
Db	1574	 TTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	 ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	3363
Db	1694	 TGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGT	1753
Qy	3364	AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	3423
Db	1754	 AGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	3483
Db	1814	 GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	3543
Db	1874	 TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	3603
Db	1934	 TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	 CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053
Qy	3664	TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	3723
Db	2054	 TGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	3783
Db	2114	 GGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCAT	2173
Qy	3784	CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	3843
Db	2174	 CATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACA	2233
Qy	3844	ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	3903
Db	2234	 ATTGTCCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA	3963

Db 2294 CAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAA 2353
 Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 4023
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGT 2413
 Qy 4024 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 4083
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2414 AACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAA 2473
 Qy 4084 AATAAAAGTTTACAGAAACCTT 4105
 ||||||||||||||
 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 10

AAF20903

ID AAF20903 standard; DNA; 1868 BP.

XX

AC AAF20903;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide #2470.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

XX

PD 26-OCT-2000.

XX

PF 24-MAR-2000; 2000WO-US08020.

XX

PR 06-APR-1999; 99US-0127958.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -

XX

PS Disclosure; Page 676; 1592pp; English.

XX

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

XX

SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 1868;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy 421 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 480

Db 10 AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT 69

Qy 481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540

Db 70 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTGTGGATGTGTAAT 129

Qy 541 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCCACCAC 600

Db 130 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTTCAACCAC 189

Qy 601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 660

Db 190 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT 249

Qy 661 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 720

Db 250 ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT 309

Qy	721	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	310	CAAATACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	370	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	429
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	549
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	610	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1149

DE Human endothelin receptor A polynucleotide fragment #2482.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 244; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or

Db	610	TAGTGTGGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAAC'TGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAAC'TGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTCCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1390	AATCCTCTCGGAGAAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509

Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATG	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1859

RESULT 12

AAA34781

ID AAA34781 standard; DNA; 1868 BP.

XX

AC AAA34781;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2470.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

[illegible]

Db	190	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	249
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAAATTACTTCAGCTTT	720
Db	250	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAAATTACTTCAGCTTT	309
Qy	721	CAAATACATTAACTGTGTATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	310	CAAATACATTAACTGTGTATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGC	369
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	370	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	429
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	430	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	489
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAAATGACTTTGGCGTATTTCTTTGCAA	960
Db	490	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAAATGACTTTGGCGTATTTCTTTGCAA	549
Qy	961	GCTGTTCCCTTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	550	GCTGTTCCCTTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	609
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	1080
Db	610	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTGAGGAATTGGGATTCC	669
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCCTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCCTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAGATGGACAAGAA	1089

XX
 AC AAA34793;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2482.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure; Page 645-646; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present

Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	670	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	729
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	730	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	789
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	790	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	849
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	850	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	909
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	969
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Db	970	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1029
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1089
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1090	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1150	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1209
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1210	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1269
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1270	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1329
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1390	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1450	CTTCTTCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1509

Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1510	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1569
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1570	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1629
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATG	2099
Db	1630	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATG	1689
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCCACCATGAAACTTTA	2159
Db	1690	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCCACCATGAAACTTTA	1749
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1750	GAGATTAACGACAAGATTTTCTACTTTTTTTTAAAGTGATTTTTTTGTCTTCAGCCAAACA	1809
Qy	2219	CAATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTGGTGCCAGTAT	2268
Db	1810	CAATATGGGCTCAAGTCACCTTTTATTTGAAATGTCATTGGTGCCAGTAT	1859

AAF20904

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PI

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CC

SO

— 22 —

Best Local

Best Local Similarity
Matches: 1844: 100%

Matches 1844; Conservative

99.7%.

Score 1815.0,
Prod No 0.

DD 21,

Height

2008,

55.7%,
five

PRED. NO. 0;
Mistake

7-1-1

D

Live

; Mismatches

4;

ndels

2; 0

aps

i

21

Db	270	 CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	329
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	330	 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	389
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	390	 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	449
Qy	721	CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	450	 CAAATACATTAACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	509
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	510	 AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	569
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	570	 AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	629
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	630	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	689
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	690	 GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	749
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	750	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	809
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140
Db	810	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	869
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	870	 TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	929
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	930	 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	989
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	990	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1049
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1050	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1109
Qy	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGGCTCTTTGCTG	1440

Db	1110	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1169
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1170	GTTCCCTCTTCATTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1229
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1560
Db	1230	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAAC	1289
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1290	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1349
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1350	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1409
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACACGATCAAAACAACCACAACACAGACCG	1740
Db	1410	CATGAACGGAACAAGCATCCAGTGAAGAACACGATCAAAACAACCACAACACAGACCG	1469
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1470	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1529
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1530	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1589
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1590	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1649
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1650	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1709
Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1710	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGAGCTGGGGGAGAATGAAGACTGT	1769
Qy	2040	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	2099
Db	1770	TAAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATG	1829
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAAATGTTCAATGGGAACTGGTCACCATGAAACTTTA	2159
Db	1830	GCTAGCTTTTATGGCAGTTCTGGTGAAATGTTCAATGGGAACTGGTCACCATGAAACTTTA	1889
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1890	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTTGTCTTCAGCCAAACA	1949
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Db	1950	CAATATGGGCTCAAGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1999

RESULT 15

AAA34782

ID AAA34782 standard; DNA; 2008 BP.

XX

AC AAA34782;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2471.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

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PN WO200009525-A2.

XX

PD 24-FEB-2000.

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PF 03-AUG-1999; 99WO-US17712.

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PR 03-AUG-1998; 98US-0095212.

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PA (UYEC-) UNIV EAST CAROLINA.

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PI Nyce JW;

XX

DR WPI; 2000-205971/18.

XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

XX

PS Disclosure; Page 607; 1343pp; English.

XX

CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX

SQ Sequence 2008 BP; 563 A; 463 C; 416 G; 566 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 2008;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	480
Db	150	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	209
Qy	481	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	210	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	269
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	600
Db	270	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCAC	329
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	330	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	389
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	390	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	449
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	450	CAAATACATTAACACTGTGATATCTTGTAATTTTCATCGTGGGAATGGTGGGGAATGC	509
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	510	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	569
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	570	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	629
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	630	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	689
Qy	961	GCTGTTCCCTTTTTCAGAAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020

Db	690	GCTGTTCCCTTTTTGCAGAAAGTCCTCGGTGGGGATCACCGTCTCAACCTCTGCGCTCT	749
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGGAATTGGGATTCC	1080
Db	750	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTACAGGGAATTGGGATTCC	809
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	810	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	869
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	870	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	929
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	930	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	989
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCCTCATGAC	1320
Db	990	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCCTCATGAC	1049
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1050	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1109
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1110	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1169
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1170	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAGATGGACAAGAA	1229
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1230	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1289
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1290	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1349
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1350	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1409
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1410	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1469
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1470	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1529
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1530	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1589

Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
Db	1590	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAAGGGTAG	1649
Qy	1920	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1979
Db	1650	ACTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACAT	1709
Qy	1980	ATTCTGCGTGTTGTATTCACTACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
Db	1710	ATTCTGCGTGTTGTATTCACTACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	1769
Qy	2040	TAAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATG	2099
Db	1770	TAAATGAAACCGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAAGTACATG	1829
Qy	2100	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTA	2159
Db	1830	GCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAAGTGGTCACCATGAAACTTTA	1889
Qy	2160	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA-TTTTTTGTCTTCAGCCAAACA	2218
Db	1890	GAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTTGTCTTCAGCCAAACA	1949
Qy	2219	CAATATGGGCTCAGGTCACTTTTATTGAAATGTCATTGGTGCCAGTAT	2268
Db	1950	CAATATGGGCTCAAGTCACTTTTATTGAAATGTCATTGGTGCCAGTAT	1999

Search completed: December 12, 2003, 11:27:08
Job time : 960.825 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:57 ; Search time 14402.7 Seconds
(without alignments)
11659.930 Million cell updates/sec

Title: US-09-931-157-1
Perfect score: 4105
Sequence: 1 gaattcgcgccgcctcttg.....taaaagtttacagaaacctt 4105

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :: GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
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- 14: gb_vi:*
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- 20: em_om:*
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28: em_un:*
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 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%	Query										
No.	Score	Match	Length	DB	ID	Description								
1	4105	100.0	4105	6	AR177879	AR177879 Sequence								
2	4105	100.0	4105	6	AX548830	AX548830 Sequence								
3	4105	100.0	4105	6	AX587759	AX587759 Sequence								
4	4105	100.0	4105	6	E07649	E07649 cDNA encodi								
5	4105	100.0	4105	9	HSET1R	X61950 H.sapiens m								
6	4103	100.0	4105	9	S57498	S57498 endothelin								
7	4101	99.9	4101	9	HUMETN1R	D90348 Homo sapien								
8	4079	99.4	4079	6	AR270694	AR270694 Sequence								
9	3183.2	77.5	3305	9	S45956	S45956 endothelin								
10	2609.6	63.6	2705	9	BC022511	BC022511 Homo sapi								
11	2470	60.2	2595	6	BD169895	BD169895 Method fo								
12	2470	60.2	2595	9	D11144S8	D11151 Homo sapien								
13	2409.2	58.7	164920	9	AC093908	AC093908 Homo sapi								
14	2292	55.8	2337	11	G06463	G06463 human STS W								
15	1819.6	44.3	1868	9	S63938	S63938 A-type endo								
16	1786.6	43.5	3216	4	BTBETREC	X57765 Bovine mRNA								
17	1560.2	38.0	1661	9	S67127	S67127 endothelin								
18	1359	33.1	1359	9	S81539	S81539 endothelin-								
19	1296.8	31.6	1310	9	HUMEDNRA	L06622 Homo sapien								
20	1280.8	31.2	1284	6	AX280871	AX280871 Sequence								
21	1280.8	31.2	1284	9	AY275462	AY275462 Homo sapi								
22	1122	27.3	1374	4	S80652	S80652 endothelin								
23	1103.2	26.9	1284	4	AF416703	AF416703 Ovis arie								
24	1088.2	26.5	2696	10	BC008277	BC008277 Mus muscu								
25	1048.8	25.5	1180	4	AF311974	AF311974 Oryctolag								
26	1021	24.9	1021	11	G10643	G10643 human STS C								
27	997	24.3	1436	10	RATENDOR	M60786 Rat endothe								
28	951	23.2	1160	9	S81542	S81542 endothelin-								
29	765.8	18.7	2944	5	AF040634	AF040634 Gallus ga								
30	765.8	18.7	2988	5	AF472618	AF472618 Gallus ga								
31	695	16.9	1032	9	S81545	S81545 endothelin-								
32	635	15.5	3767	5	BC044316	BC044316 Xenopus l								
33	632.8	15.4	1650	5	XLU06633	U06633 Xenopus lae								

	34	624.6	15.2	810	10	AF039892	AF039892 Mus muscu
	35	514	12.5	530	9	MFU20577	U20577 Macaca fasc
	36	492.4	12.0	531	9	D11144S2	D11145 Homo sapien
	37	487.4	11.9	1435	9	S55547S2	S55772 ETA=endothe
c	38	487.4	11.9	66264	2	AC110065	AC110065 Homo sapi
	39	435.6	10.6	3157	5	BC048223	BC048223 Xenopus l
	40	425	10.4	1308	5	CCEDNRB2	Y16089 Coturnix co
	41	423.4	10.3	2225	5	AF472617	AF472617 Gallus ga
	42	411.6	10.0	1724	5	AB045356	AB045356 Oryzias l
	43	411	10.0	1314	4	AF276427	AF276427 Canis fam
	44	407.8	9.9	1311	4	AF038900	AF038900 Equus cab
	45	407.8	9.9	1452	4	AF034530	AF034530 Canis fam

ALIGNMENTS

RESULT 1

AR177879

LOCUS AR177879 4105 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 1 from patent US 6313276.

ACCESSION AR177879

VERSION AR177879.1 GI:17920234

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Imura,H., Nakao,K. and Nakanishi,S.

TITLE Human endothelin receptor

JOURNAL Patent: US 6313276-A 1 06-NOV-2001;

FEATURES Location/Qualifiers

source 1..4105

/organism="unknown"

BASE COUNT 1138 a 859 c 845 g 1263 t

ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCGCGGCCGCTCTTGC	CGTCCCAGAGTGGAGTGG	AAGTCTGGAGCTTTGGG	GAGG 60
Db	1	GAATTCGCGGCCGCTCTTGC	CGTCCCAGAGTGGAGTGG	AAGTCTGGAGCTTTGGG	GAGG 60
Qy	61	AGACGGGGAGGACAGACTGG	AGGCGTGTTCTCCGGAGT	TTTTCTTTTTCGTGCGAG	CCCT 120
Db	61	AGACGGGGAGGACAGACTGG	AGGCGTGTTCTCCGGAGT	TTTTCTTTTTCGTGCGAG	CCCT 120
Qy	121	CGCGCGCGCGTACAGTCAT	CCCGCTGGTCTGACGATT	GTGGAGAGGCGGTGGAG	AGGCTT 180
Db	121	CGCGCGCGCGTACAGTCAT	CCCGCTGGTCTGACGATT	GTGGAGAGGCGGTGGAG	AGGCTT 180
Qy	181	CATCCATCCCACCCGGTCG	TGCGCCGGGGATTGGGGT	CCCAGCGACACCTCCCC	GGGAGAA 240
Db	181	CATCCATCCCACCCGGTCG	TGCGCCGGGGATTGGGGT	CCCAGCGACACCTCCCC	GGGAGAA 240

Qy	241	GCAGTGCCCAAGGATTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAAGGATTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCCGGGACACCGGCCACCCTCCGCGCCACCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCCGGGACACCGGCCACCCTCCGCGCCACCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCTCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTAGGGAATTGGGATTCC	1080
Qy	1081	TTTGTTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCCTTTATCCTGGCCATTCC	1140

Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980

Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820

Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Db	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660

Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAAGTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAGTTTACAGAAACCTT	4105

RESULT 2

AX548830

LOCUS AX548830 4105 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 115 from Patent WO02061087.

ACCESSION AX548830

VERSION AX548830.1 GI:25813724

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides

JOURNAL Patent: WO 02061087-A 115 08-AUG-2002;

Lifespan Biosciences, Inc. (US)

FEATURES

source

Location/Qualifiers

1. .4105

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 1138 a 859 c 845 g 1263 t

ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Db	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCGAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCGAGGAAGTTTTCTGAAGCCGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCGAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCAAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCAAAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACACTGTGATATCTTGTAATTTTTTCATCGTGGGAATGGTGGGGAATGC	780

Qy	781	AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACAGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Db	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620

Qy	1621	TTTCCAGTCAATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCAATGCCTCTGCTGCTGCTGTTACCAAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGGAAGAACACGATCAAAAACAACCAACACAGACCG	1740
Db	1681	CATGAACGGAACAAGCATCCAGTGGGAAGAACACGATCAAAAACAACCAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCACACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTTATTTTTTAA	2520

Db	2461	 TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	 ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Db	2581	 TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Db	2641	 AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Db	2701	 TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	 ATGATTTCGGAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Db	2821	 CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	 TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	 GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Db	3001	 TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Db	3061	 GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
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Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	 ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	 GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360

Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Qy	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
Qy	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Db	3901	ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG	3960
Qy	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Db	3961	TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA	4020
Qy	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Db	4021	AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG	4080
Qy	4081	TAAAATAAAAAGTTTACAGAAACCTT	4105
Db	4081	TAAAATAAAAAGTTTACAGAAACCTT	4105

LOCUS AX587759 4105 bp DNA linear PAT 10-JAN-2003
 DEFINITION Sequence 229 from Patent WO0246467.
 ACCESSION AX587759
 VERSION AX587759.1 GI:28212399
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and
 Fert,V.
 TITLE Gene expression profiling of primary breast carcinomas using arrays
 of candidate genes
 JOURNAL Patent: WO 0246467-A 229 13-JUN-2002;
 Ipsogen (FR)
 FEATURES Location/Qualifiers
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 misc_feature 1. .4105
 /note="endothelin receptor type a (EDNRA) gene."
 BASE COUNT 1138 a 859 c 845 g 1263 t
 ORIGIN

Query Match 100.0%; Score 4105; DB 6; Length 4105;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	GAATTCGCGGCCGCTCTTGCGGTCCCAGAGTGGAGTGGGAAGGTCTGGAGCTTTGGGAGG	60
Qy	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTCGAGCCCT	120
Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTCGAGCCCT	120
Qy	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
Db	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420

Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGCAATAAGAGATATTTTCCTCAAATTTGCCT	480
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Qy	481	CAAGATGGAAACCCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
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Qy	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
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Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
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Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Db	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCTTTTTTGAGAAAGTCCCGGTGGGGATCACCGTCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAAGTCCCGGTGGGGATCACCGTCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACGGGAATTGGGATTCC	1080
Db	1021	TAGTGTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTTACGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320

Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
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Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681	 CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	 GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	 AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861	 CTTCTTCCTTAATTCACTCCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	 CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTACAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	 TTCTGCGTGTTGTATTACAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	 AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160

Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTTAA	2400
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Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
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Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
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Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
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Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
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Qy	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
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Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
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Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTTGGGGTTT	3000
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Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCAACCATTTTCAAAG	3060
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Qy	3061	GGCCACACAGTGACTTTTGGCTGGGCATTTTCCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
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Qy	3121	AAAATCTTTTACTAGTGTGTGTGTGTATATATATAAAACAATTGTAAATTTCTTTTAGCCC	3180
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Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
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Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGCAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTTCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
Qy	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Db	3421	AGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACCTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Db	3541	CACCTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGT	3600
Qy	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Db	3601	TGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
Qy	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
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Db	3721	CAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCG	3780
Qy	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAG	3840
Db	3781	CATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTTCACACCATTTTGTTTAG	3840

Qy 3841 ACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAA 3900
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Qy 3901 ATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAG 3960
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Qy 3961 TAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACA 4020
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Qy 4021 AGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTG 4080
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RESULT 4

E07649

LOCUS E07649 4105 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding endothelin receptor, ETA-receptor.

ACCESSION E07649

VERSION E07649.1 GI:2175784

KEYWORDS JP 1994157595-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Imura, H., Nakao, I. and Nakanishi, S.

TITLE HUMAN ENDOTHELIN RECEPTOR

JOURNAL Patent: JP 1994157595-A 1 03-JUN-1994;
 SHIONOGI & CO LTD

COMMENT OS Homo sapiens (human)

PN JP 1994157595-A/1

PD 03-JUN-1994

PF 12-JUL-1991 JP 1991172828

PI IMURA HIROO, NAKAO ICHIKAZU, NAKANISHI SHIGETADA PC

C07K13/00, C12N5/10, C12N15/12, C12P21/02, (C12N5/10, C12R1:91), PC
 (C12P21/02,

PC C12R1:91);

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

FH Key Location/Qualifiers

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FT /tissue_type='placenta'

FT /clone='phETIR'

FT 5'UTR 1. .484

FT CDS 485. .1768

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Best Local Similarity 100.0%;  Pred. No. 0;
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Qy    121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
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Qy    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240
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Db    181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

Qy    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC 300
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Db    241 GCAGTGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCCGCGC 300

Qy    301 CGGAGCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC 360
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Qy    481 CAAGATGGAAACCCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT 540
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Qy	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTT	660
Db	601	TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGACTATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
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Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
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Qy	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	GCTGTTCCCTTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Db	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAAGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	TGAAGCGATTGGCTTCGTATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTG	1440

Db	1381		GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTG	1440
Qy	1441		GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441		GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501		CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501		CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561		CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561		CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621		TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621		TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681		CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Db	1681		CATGAACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741		GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741		GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801		AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801		AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861		CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Db	1861		CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGA	1920
Qy	1921		CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921		CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
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Qy	2041		AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
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Qy	2101		CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
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Qy	2161		AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
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Qy	2221		ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280

Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAAA	2400
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Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTGTATGA	2640
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Qy	2761	ATGATTTCGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
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Qy	2821	CACCTCCTATTCTCTTAATTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
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Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
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Db	3601	TGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATA	3660
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Db	3661	ATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTG	3720
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Qy	3781	CATCATATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAG	3840
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RESULT 5

HSET1R

LOCUS HSET1R 4105 bp mRNA linear PRI 23-MAR-1993

DEFINITION H.sapiens mRNA for endothelin-1 receptor.

ACCESSION X61950

VERSION X61950.1 GI:288312

KEYWORDS endothelin-1 receptor.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Hosoda,K., Nakao,K., Hiroshi-Arai, Suga,S., Ogawa,Y., Mukoyama,M.,
 Shirakami,G., Saito,Y., Nakanishi,S. and Imura,H.

TITLE Cloning and expression of human endothelin-1 receptor cDNA

JOURNAL FEBS Lett. 287 (1-2), 23-26 (1991)

MEDLINE 91348221

PUBMED 1652463

FEATURES

source

Location/Qualifiers

1. .4105

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485. .1768

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BASE COUNT 1138 a 859 c 845 g 1263 t

ORIGIN

Query Match 100.0%; Score 4105; DB 9; Length 4105;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	AGACGGGGAGGACAGACTGGAGGCGTGTTCTCCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT	120
Qy	121	CGCGCGCGGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Db	121	CGCGCGCGGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT	180
Qy	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Db	181	CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA	240
Qy	241	GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Db	241	GCAGTGCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCGC	300
Qy	301	CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC	360
Db	301	CGGAGCCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCCTC	360
Qy	361	TGGCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
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Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCT	480
Qy	481	CAAGATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Db	481	CAAGATGGAAACCTTTGCCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCAC	600
Qy	601	TTTTCTGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Db	601	TTTTCTGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAATTACTTCAGCTTT	720
Qy	721	CAAATACATTAACTGTGATATCTTGTAATATTTTCATCGTGGGAATGGTGGGGAATGC	780
Db	721	CAAATACATTAACTGTGATATCTTGTAATATTTTCATCGTGGGAATGGTGGGGAATGC	780
Qy	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCAACGCGCTGAT	840
Db	781	AACTCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCAACGCGCTGAT	840
Qy	841	AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900

Db	841	 AGCCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATT	900
Qy	901	TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Db	901	 TAAGCTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAA	960
Qy	961	GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	961	 GCTGTTCCCCTTTTTGCAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Db	1021	 TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Db	1081	 TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Db	1141	 TGAAGCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	 TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Db	1261	 CTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	 TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTG	1440
Db	1381	 GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTG	1440
Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Db	1441	 GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAA	1500
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Db	1501	 CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1560
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	 CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	 TTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACAAGCATCCAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740

Db	1681	CATGAACGGAACAAGCATCCAGTGGGAAGAACCACGATCAAAACAACCACAACACAGACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGA	1920
Db	1861	CTTCTTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCAAAACCGCAAGGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATA	1980
Qy	1981	TTCTGCGTGTTGTATTCACTACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTTGTATTCACTACTAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Db	2041	AAATGAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAG	2160
Qy	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Db	2161	AGATTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTAA	2400
Qy	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAA	2520
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Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGC	2580

Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGA	2640
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Qy	2641	AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTT	2700
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Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Db	2701	TCAGTGCACTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAG	2760
Qy	2761	ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTTCGGAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTTTGTTAAAATGTTAACTGGCAGTAAGTCTTTTTTGATCA	2880
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Qy	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Db	2881	TTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
Qy	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACTTCTTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Db	3001	TCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCACATTGTCACCATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTTGCTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
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Qy	3121	AAAATCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCC	3180
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Qy	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Db	3181	ATTTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGAT	3240
Qy	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Db	3241	GGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATA	3300
Qy	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Db	3301	GTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATA	3420
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RESULT 6

S57498

LOCUS S57498 4105 bp mRNA linear PRI 29-JAN-2002

DEFINITION endothelin ET-A receptor [human, mRNA, 4105 nt].

ACCESSION S57498

VERSION S57498.1 GI:298319

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4105)

AUTHORS Arai,H., Nakao,K., Hosoda,K., Ogawa,Y., Nakagawa,O., Komatsu,Y. and Imura,H.

TITLE Molecular cloning of human endothelin receptors and their expression in vascular endothelial cells and smooth muscle cells

JOURNAL Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)

MEDLINE 93180293

PUBMED 1291713

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 128422] from the original journal article. This sequence comes from Fig. 5.

FEATURES

Location/Qualifiers

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 PEAIGFVMVPFEYRGEQHKTCMLNATSKFMEFYQDVKDWWLFGFYFCMPLVCTAIFYT
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BASE COUNT 1138 a 859 c 843 g 1263 t 2 others

ORIGIN

Query Match 100.0%; Score 4103; DB 9; Length 4105;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GAATTCGCGGCCCGCCTCTTGCGGTCCCAGAGTGGAGTGAAGGTCTGGAGCTTTGGGAGG 60

Qy 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT 120
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Db 61 AGACGGGGAGGACAGACTGGAGGCGTGTTCCTCCGGAGTTTTCTTTTTCTGTGCGAGCCCT 120

Qy 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180
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Db 121 CGCGCGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTT 180

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Db 181 CATCCATCCCACCCGGTCGTCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAA 240

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Qy	301	CGGAGCCCCGGGACACCGGCCACCCTCCGCGCCACCCACCCTCGCTTTCTCCGGCTTCCTC	360
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Qy	361	TGGCCCAGGCGCCGCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAA	420
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Qy	421	AAAAAGTGAAGGTGTAAAAGCAGCACAAAGTGAATAAGAGATATTTCTCAAATTTGCCT	480
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Qy	481	CAAGATGGAAACCTTTTGCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAAT	540
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Qy	1021	TAGTGTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCC	1080
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Qy	1081	TTTGGTAACTGCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCC	1140
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Qy	1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTGAACAGAANNAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAGTGGCAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTG	1440
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Qy	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAA	1500
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Qy	1561	CATGAATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
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RESULT 7

HUMETN1R

LOCUS HUMETN1R 4101 bp mRNA linear PRI 18-DEC-2002

DEFINITION Homo sapiens mRNA for endothelin-1 receptor, complete cds.

ACCESSION D90348

VERSION D90348.1 GI:219649

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4101)

AUTHORS Hosoda,K., Nakao,K., Hiroshi-Arai, Suga,S., Ogawa,Y., Mukoyama,M.,
 Shirakami,G., Saito,Y., Nakanishi,S. and Imura,H.

TITLE Cloning and expression of human endothelin-1 receptor cDNA

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COMMENT These data kindly submitted in computer readable form by: Kazuwa
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FEATURES             Location/Qualifiers
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BASE COUNT      1136 a      859 c      844 g      1262 t
ORIGIN

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Query Match 99.9%; Score 4101; DB 9; Length 4101;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
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Qy	1385	CGTCGAGAAGTGGCAAAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	1444
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Qy	1565	AATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
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Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
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Qy	1985	GCGTGTGTGATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
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Db	3361	GCAACCTTCTGCATTCTATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
Qy	3485	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3544
Db	3481	TTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACT	3540
Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
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Qy	3665	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3724
Db	3661	GTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAG	3720
Qy	3725	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3784
Db	3721	GCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATC	3780
Qy	3785	ATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAA	3844
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Qy	3845	TTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTC	3904
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Qy	3905	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3964
Db	3901	AGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAC	3960
Qy	3965	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4024
Db	3961	TGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTA	4020
Qy	4025	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAAG	4084
Db	4021	ACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAAG	4080
Qy	4085	ATAAAAGTTTACAGAAACCTT	4105
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RESULT 8

AR270694

LOCUS AR270694 4079 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 1257 from patent US 6500938.

ACCESSION AR270694

VERSION AR270694.1 GI:29701928

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 4079)

AUTHORS Au-Young, J. and Seilhamer, J.J.

TITLE Composition for the detection of signaling pathway gene expression

JOURNAL Patent: US 6500938-A 1257 31-DEC-2002;

FEATURES Location/Qualifiers

source 1. .4079

/organism="unknown"

BASE COUNT 1125 a 856 c 842 g 1256 t

ORIGIN

Query Match 99.4%; Score 4079; DB 6; Length 4079;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	65	GGGGAGGACAGACTGGAGGCGTGTTCCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCTCGCG	124
Db	61	GGGGAGGACAGACTGGAGGCGTGTTCCCTCCGAGTTTTCTTTTTCTGTGCGAGCCCTCGCG	120
Qy	125	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	184
Db	121	CGCGCGTACAGTCATCCCGCTGGTCTGACGATTGTGGAGAGGCGGTGGAGAGGCTTCATC	180

Qy	185	CATCCCACCCGGTTCGTCCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG	244
Db	181	CATCCCACCCGGTTCGTCCGCCGGGGATTGGGGTCCCAGCGACACCTCCCCGGGAGAAGCAG	240
Qy	245	TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	304
Db	241	TGCCCAGGAAGTTTTCTGAAGCCGGGGAAGCTGTGCAGCCGAAGCCGCCGCCGCCGGA	300
Qy	305	GCCCCGGGACACCGGCCACCCTCCGCGCCACCACCCCTCGCTTTCTCCGGCTTCCTCTGGC	364
Db	301	GCCCCGGGACACCGGCCACCCTCCGCGCCACCACCCCTCGCTTTCTCCGGCTTCCTCTGGC	360
Qy	365	CCAGGCGCCGCCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAA	424
Db	361	CCAGGCGCCGCCGCGGACCCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAA	420
Qy	425	AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG	484
Db	421	AGTGAAGGTGTAAAAGCAGCACAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAG	480
Qy	485	ATGGAAACCCTTTGCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	544
Db	481	ATGGAAACCCTTTGCTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGT	540
Qy	545	GATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCACTTTT	604
Db	541	GATAATCCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTACCACTTTT	600
Qy	605	CGTGGCACAGAGCTCAGCTTCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCC	664
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Qy	665	AGCAATGGCTCAATGCACAACCTATTGCCACAGCAGACTAAAACTTCTCAGCTTTCAA	724
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Db	721	TACATTAACACTGTGATATCTTGTACTATTTTCATCGTGGGAATGGTGGGGAATGCAACT	780
Qy	785	CTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	844
Db	781	CTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCC	840
Qy	845	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	904
Db	841	AGTCTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAG	900
Qy	905	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	964
Db	901	CTGCTGGCTGGGCGCTGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTG	960
Qy	965	TTCCCCTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1024
Db	961	TTCCCCTTTTTGAGAAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGT	1020

Qy	1025	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCTTTTG	1084
Db	1021	GTTGACAGGTACAGAGCAGTTGCCTCCTGGAGTCGTGTTCAGGGAATTGGGATTCTTTTG	1080
Qy	1085	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1144
Db	1081	GTAAGTCCATTGAAATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAA	1140
Qy	1145	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATG	1204
Db	1141	GCGATTGGCTTCGTTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATG	1200
Qy	1205	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1264
Db	1201	CTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTC	1260
Qy	1265	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGACTTGT	1324
Db	1261	GGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGCGATCTTCTACACCTCATGACTTGT	1320
Qy	1325	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1384
Db	1321	GAGATGTTGAACAGAAGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG	1380
Qy	1385	CGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	1444
Db	1381	CGTCGAGAAGTGGCAAAACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTC	1440
Qy	1445	CCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAACCGA	1504
Db	1441	CCTCTTCACTTAAGCCGTATATTGAAGAAACTGTGTATAACGAAATGGACAAGAACCGA	1500
Qy	1505	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1564
Db	1501	TGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAACCATG	1560
Qy	1565	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1624
Db	1561	AATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTC	1620
Qy	1625	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1684
Db	1621	CAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATG	1680
Qy	1685	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1744
Db	1681	AACGGAACAAGCATCCAGTGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGC	1740
Qy	1745	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATATC	1804
Db	1741	AGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATATC	1800
Qy	1805	CTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1864
Db	1801	CTCTCGGAGAAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTC	1860
Qy	1865	TTCCTTAATTCACCTCCACACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1924

Db	1861	 TTCCTTAATTCACTCCCAACCCAAGAAGAAATGCTTTCCAAAACCGCAAGGTAGACTGG	1920
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Db	1921	 TTTATCCACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCT	1980
Qy	1985	GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2044
Db	1981	 GCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAAT	2040
Qy	2045	GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2104
Db	2041	 GAAACCAGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAG	2100
Qy	2105	CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2164
Db	2101	 CTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAGAT	2160
Qy	2165	TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2224
Db	2161	 TAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATAT	2220
Qy	2225	GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2284
Db	2221	 GGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCATAAT	2280
Qy	2285	AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAATA	2344
Db	2281	 AGCCTAACATGATTATTTGAACTTATTTACACATAGTTTGAAAAAAAAAAGACAAAATA	2340
Qy	2345	GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACAC	2404
Db	2341	 GTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAACAC	2400
Qy	2405	AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2464
Db	2401	 AAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTTG	2460
Qy	2465	GCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGG	2524
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Db	2521	 TGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTCA	2580
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Qy	3005	TATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTGTCAACATTTCAAAGGGCC	3064
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Qy	3125	TCTTTTACTAGTGTGTGTGTATATATATAAACAATTGTAAATTTCTTTTAGCCCATTT	3184
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Db	3181	TTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTGATATATGCATGTGTGTGATGGTA	3240
Qy	3245	TGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATAGTCT	3304
Db	3241	TGTATGGATTTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATAGTCT	3300
Qy	3305	GAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTA	3364
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Qy	3365	GCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3424
Db	3361	GCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAG	3420
Qy	3425	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3484
Db	3421	GCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGT	3480
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Qy	3545	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3604
Db	3541	TTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTC	3600

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RESULT 9

S45956

LOCUS S45956 3305 bp mRNA linear PRI 08-MAY-1993

DEFINITION endothelin receptor subtype A [human, placenta, mRNA, 3305 nt].

ACCESSION S45956

VERSION S45956.1 GI:257375

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3305)

AUTHORS Hayzer,D.J., Rose,P.M., Lynch,J.S., Webb,M.L., Kienzle,B.K.,
 Liu,E.C., Bogosian,E.A., Brinson,E. and Runge,M.S.

TITLE Cloning and expression of a human endothelin receptor: subtype A

JOURNAL Am. J. Med. Sci. 304 (4), 231-238 (1992)

MEDLINE 93035452

PUBMED 1415318

REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gibbsq 115436] from the original journal article.

This sequence comes from Fig. 2.

FEATURES Location/Qualifiers

source 1..3305


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ORIGIN

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Query Match          77.5%; Score 3183.2; DB 9; Length 3305;
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Qy	983	TCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCA	1042
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Qy	1043	GTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATT	1102
Db	780	GTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAATT	839
Qy	1103	GTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATG	1162
Db	840	GTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATG	899
Qy	1163	GTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCCACATCAAAA	1222
Db	900	GTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCCACATCAAAA	959
Qy	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Db	960	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1019
Qy	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Db	1020	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1079
Qy	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Db	1080	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1139
Qy	1403	ACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Db	1140	ACAGTTTTCTGCTTGGTTGTAATTTTGTCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1199
Qy	1463	ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Db	1200	ATATTGAAGAAAACCTGTGTATAACGAGATGGACAAGAACCGATGTGAATTACTTAGTTTC	1259
Qy	1523	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1582
Db	1260	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1319

Qy	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Db	1320	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1379
Qy	1643	TGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAG	1702
Db	1380	TGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAG	1439
Qy	1703	TGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATG	1762
Db	1440	TGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATG	1499
Qy	1763	AACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATCCTCTCGGAGAAAAAATC	1822
Db	1500	AACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCATAAATCCTCTCGGAGAAAAAATC	1559
Qy	1823	ACAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCA	1882
Db	1560	ACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCA	1619
Qy	1883	CACCCAAGAAGAAATGCTTTTCCAAAACCGCAA - GGTAGACTGGTTTATCCACCCACAACA	1941
Db	1620	CACCCAAGAAGAAATGCTTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACA	1679
Qy	1942	TCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCA	2001
Db	1680	TCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCA	1739
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Qy	2062	TACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTG	2121
Db	1800	TACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTCCTG	1859
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Db	2220	TACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGG	2279
Qy	2541	ACCTTGAACATGTTTTGTATGTTAAATTCAAAAGTAATGCTTCAATCAGATAGTTCTTTT	2600
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Db	2638	ACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAATTACCCACAAA	2697
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RESULT 10

BC022511

LOCUS BC022511 2705 bp mRNA linear PRI 04-FEB-2002

DEFINITION Homo sapiens, endothelin receptor type A, clone MGC:26548

IMAGE:4812050, mRNA, complete cds.

ACCESSION BC022511

VERSION BC022511.1 GI:18490297

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2705)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 32 Row: j Column: 7
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503464.

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FEATURES             Location/Qualifiers
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                        /note="Vector: pBluescript"
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BASE COUNT          767 a    594 c    560 g    784 t
ORIGIN

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Query Match 63.6%; Score 2609.6; DB 9; Length 2705;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 2673; Conservative 0; Mismatches 14; Indels 5; Gaps 5;

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Qy	674		TCAATGCACAACACTATTGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAAC	733
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RESULT 11

BD169895

LOCUS BD169895 2595 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method for examination of allergosis.
 ACCESSION BD169895
 VERSION BD169895.1 GI:27875707
 KEYWORDS WO 02052006-A/28.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2595)
AUTHORS Otani,N., Matsui,K., Yoshida,N., Sugita,Y. and Izuhara,K.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 02052006-A 28 04-JUL-2002;
GENOX RESEARCH INC,NORIKO OTANI,KEIKO MATSUI,NEI YOSHIDA, YUJI
SUGITA, KENJI IZUHARA
COMMENT OS Homo sapiens (human)
PN WO 02052006-A/28
PD 04-JUL-2002
PF 21-DEC-2001 WO 2001JP011287
PR 26-DEC-2000 JP 00P 396166
PI NORIKO OTANI,KEIKO MATSUI,NEI YOSHIDA,YUJI SUGITA,KENJI PI
IZUHARA
PC C12N15/12,C12Q1/68,C12Q1/02,A01K67/027,A61K31/713,A61K45/00,
PC A61K48/00,
PC A61P37/08,G01N33/15,G01N33/50,G01N33/53
CC Method for examination of allergosis
FH Key Location/Qualifiers
FT source 1. .2595
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 788 a 478 c 459 g 870 t
ORIGIN

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Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy	2104	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	2163
Db	495	 GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	 TTAACGACAAGATTTTCTACTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
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Qy	3244	ATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTC	3303
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Db	1754	AGCAACCTTCTGCATTCTAATAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGA	1813
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Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
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Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
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RESULT 12

D11144S8

LOCUS D11144S8 2595 bp DNA linear PRI 19-SEP-2002

DEFINITION Homo sapiens gene for endothelin-A receptor, complete cds, exon 8 and 3' flanking region.

ACCESSION D11151

VERSION D11151.1 GI:219628

KEYWORDS G protein-coupled receptor; endothelium; smooth muscle.

SEGMENT 8 of 8

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2595)

AUTHORS Hosoda,K., Nakao,K., Tamura,N., Arai,H., Ogawa,Y., Suga,S., Nakanishi,S. and Imura,H.

TITLE Organization, structure, chromosomal assignment, and expression of the gene encoding the human endothelin-A receptor

JOURNAL J. Biol. Chem. 267 (26), 18797-18804 (1992)

MEDLINE 92406798

PUBMED 1326535

REFERENCE 2 (bases 1 to 2595)

AUTHORS Hosoda,K.

TITLE Direct Submission

JOURNAL Submitted (18-MAY-1992) Kiminori Hosoda, Kyoto University School of Medicine, Department of Medicine; 54 Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan (Tel:81-75-751-3170,

Fax:81-75-771-9452)

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db	435	TGAAACCAGAAGGATATTTACTACTTTTGCATGAAAAATAGAGCTTTCAGTACATGGCTA	494
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Db	495	GCTTTTATGGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAAACTTTAGAGA	554
Qy	2164	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	2223
Db	555	TTAACGACAAGATTTTCTACTTTTTTTAAGTGATTTTTTGTCTTCAGCCAAACACAATA	614
Qy	2224	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCATAA	2283
Db	615	TGGGCTCAGGTCACTTTTATTTGAAATGTCATTGGTGCCAGTATTTTTTAACTGCATAA	674
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Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACTATTTATTTTTTTAAAACA	794
Qy	2404	CAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
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Qy	2464	GGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAATG	2523
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Qy	2524	GTGTTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTTC	2583
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Qy	2584	AATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTCA	1093
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Qy	2764	ATTCGGAAATTTTCATTCAAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
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Db	1814	GGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGG	1873
Qy	3484	TTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAGTCATTACAC	3543
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Db	1934	TTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGT	1993
Qy	3604	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	3663
Db	1994	CTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATT	2053

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AC093908

LOCUS AC093908 164920 bp DNA linear PRI 01-MAR-2002

DEFINITION Homo sapiens BAC clone RP11-752L20 from 4, complete sequence.

ACCESSION AC093908 AC067873

VERSION AC093908.3 GI:18497272

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 164920)

AUTHORS Sulston,J.E. and Waterston,R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792

PUBMED 9847074

REFERENCE 2 (bases 1 to 164920)

AUTHORS Paulson,E., Cotton,M. and Creason,K.

TITLE The sequence of Homo sapiens BAC clone RP11-752L20

JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 164920)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE 4 (bases 1 to 164920)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (05-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE 5 (bases 1 to 164920)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (08-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 6 (bases 1 to 164920)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Feb 5, 2002 this sequence version replaced gi:15778805.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0752L20

Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-56F3. Actual start of this clone is at base position 1 of RP11-752L20; actual end is at base position 164920 of RP11-752L20.

Data from AC083898 was used to finish this clone, AC093908.

The sequence of AC067873 has been incorporated into AC093908.

FEATURES	Location/Qualifiers
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repeat_region	4328. .4359 /rpt_family="AT_rich"
repeat_region	4786. .4811 /rpt_family="(CA)n"
repeat_region	4813. .4874 /rpt_family="(TC)n"
repeat_region	4883. .4910 /rpt_family="(CA)n"
repeat_region	4948. .5511 /rpt_family="L1"
repeat_region	5058. .5099 /rpt_family="AT_rich"
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Best Local Similarity 99.4%;  Pred. No. 0;
Matches 2470;  Conservative 0;  Mismatches 8;  Indels 6;  Gaps 5;

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Qy      1804 CCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGAATCTCTTCTCTGATCCTT 1863
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Qy	2462	TTGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAA	2521
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Qy	2642	AAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAATTTAACTCTGCCTGAGACTTT	2701
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Qy	2762	TGATTCGGAAATTTTCATTTCAGGTATTTGTAATAGTGACATATATATGTATATACATATC	2821
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Qy	3422	GAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTT	3481
Db	95154	GAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTT	95213
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Qy	3542	ACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTT	3601
Db	95274	ACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTT	95333
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Qy	3962	AACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAA	4021
Db	95694	AACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAA	95753

Qy 4022 GTAAC TTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGT 4081
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 Db 95814 AAAATAAAAGTTTACAGAAACCTT 95837

RESULT 14

G06463

LOCUS G06463 2337 bp DNA linear STS 19-OCT-1995

DEFINITION human STS WI-7226, sequence tagged site.

ACCESSION G06463

VERSION G06463.1 GI:859708

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2337)

AUTHORS Hudson,T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically
 Mapped ESTs

JOURNAL Unpublished (1995)

COMMENT

Contact: Thomas Hudson
 Whitehead Institute/MIT Center for Genome Research
 Whitehead Institute for Biomedical Research
 9 Cambridge Center, Cambridge MA 02142 USA
 Tel: 617 252 1900
 Fax: 617 252 1902
 Email: thudson@genome.wi.mit.edu

Primer A: GATCGAATTTTTCAGATGATTTCG

Primer B: AAATGCCCAGCAAAAGTCAC

STS size: 343

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 nM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCL: 10 mM

pH: 9.3

Prepared with primer pairs derived from D90348 -- Unigene.

FEATURES Location/Qualifiers
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BASE COUNT 694 a 407 c 407 g 784 t 45 others
ORIGIN

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Db	181	ATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAA	240
Qy	2009	ATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACT	2068
Db	241	ATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACT	300
Qy	2069	TTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATG	2128
Db	301	TTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATG	360
Qy	2129	TTCAATGGGAACTGGTCACCATGAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTT	2188
Db	361	TTCAATGGGAACTGGTCACCATGAACTTTAGAGATTAACGACAAGANNNNNNNNNNNNNN	420
Qy	2189	TTAAGTGATTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAA	2248
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Qy	2249	ATGTCATTTGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTT	2308
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Qy	2309	ATTTACACATAGTTTGAAAAAAAAAAGACAAAAATAGTATTCAGGTGAGCAATTAGATTA	2368

Db	541	ATTTACACATAGTTTGNNNNNNNNNNNNNNNNNNNNTAGTATTTCAGGTGAGCAATTAGATTA	600
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Db	601	GTATTTTCCACGTCACACTATTTATTTTTTTTAAACACAAATTCTAAAGCTACAACAAATAC	660
Qy	2429	TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAA	2488
Db	661	TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAA	720
Qy	2489	GAATTTTTTAAGAACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAA	2548
Db	721	GAATTTTTTAAGAACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAA	780
Qy	2549	CATGTTTTGTATGTTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTTCACAAGT	2608
Db	781	CATGTTTTGTATGTTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTTCACAAGT	840
Qy	2609	TCAATACTGTTTTTCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAAATGTTA	2668
Db	841	TCAATACTGTTTTTCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAAATGTTA	900
Qy	2669	ATGTATGTGTCATTTAACTCTGCCTGAGACTTTTCAGTGCAGTGTATATAGAAGTCTAAAA	2728
Db	901	ATGTATGTGTCATTTAACTCTGCCTGAGACTTTTCAGTGCAGTGTATATAGAAGTCTAAAA	960
Qy	2729	CACACCTAAGAGAAAAAGATCGAATTTTTCAGATGATTCCGAAATTTTCATTTCAGGTATT	2788
Db	961	CACACCTAAGAGAAAAAGATCGAATTTTTCAGATGATTCCGAAATTTTCATTTCAGGTATT	1020
Qy	2789	TGTAATAGTGACATATATATGTATATACATATCACCTCCTATTCTCTTAATTTTGTAA	2848
Db	1021	TGTAATAGTGACATATATATGTATATACATATCACCTCCTATTCTCTTAATTTTGTAA	1080
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Db	1081	AATGTTAACTGGCAGTAAGTCTTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATT	1140
Qy	2909	TTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAATAATAATTACCCACAAATGCCACCA	2968
Db	1141	TTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAATAATAATTACCCACAAATGCCACCA	1200
Qy	2969	GTAACCTTAACGATTCTTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCCCACCCAA	3028
Db	1201	GTAACCTTAACGATTCTTCACTTCTTGGGGTTTTTCAGTATGAACCTAACTCCCCACCCAA	1260
Qy	3029	CATCTCCCTCCACATTGTCAACATTTCAAAGGGCCACAGTGACTTTTGCTGGGCATTT	3088
Db	1261	CATCTCCCTCCACATTGTCAACATTTCAAAGGGCCACAGTGACTTTTGCTGGGCATTT	1320
Qy	3089	TCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGTGTGTGTAT	3148
Db	1321	TCCCAGATGTTTACAGACTGTGAGTACAGCAGAAAATCTTTTACTAGTGTGTGTGTAT	1380
Qy	3149	ATATATAAACAATTGTAAATTTCTTTTAGCCCATTTTTCTAGACTGTCTCTGTGGAATAT	3208
Db	1381	ATATATAAACAATTGTAAATTTCTTTTAGCCCATTTTTCTAGACTGTCTCTGTGGAATAT	1440

Qy	3209	ATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAATCTAATCTAAT	3268
Db	1441	ATTTGTGTGTGTGATATATGCATGTGTGTGATGGTATGTATGGATTTAATCTAATCTAAT	1500
Qy	3269	AATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTCTGAGCTAAAATCTAGGTGATTGTTC	3328
Db	1501	AATTGTGCCCCGAGTTGTGCCAAAGTGCATAGTCTGAGCTAAAATCTAGGTGATTGTTC	1560
Qy	3329	ATCATGACAACCTGCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCATTCTATAAATCT	3388
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Qy	3389	TGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGT	3448
Db	1621	TGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGT	1680
Qy	3449	GGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCA	3508
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Qy	3689	AAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTG	3748
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Qy	3749	TGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAA	3808
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Db	1090	CCGATGTGAATTACTTAGTTTTCTTACTGCTCATGGATTACATCGGTATTAACTTGGCAAC	1149
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTG	1620
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Qy	1741	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1330	GAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAGAAGCACTCCTCGGTACTCCCAT	1389
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Db	1390	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAGTCCGGGAATCTCTTCTCTGATC	1449
Qy	1861	CTTCTTCCTTAATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAAACCGCAA-GGTAG	1919
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Qy	1980	ATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGT	2039
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Search completed: December 12, 2003, 19:39:03
Job time : 14421.7 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:17:01 ; Search time 7395.45 Seconds
(without alignments)
13490.718 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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2: em_esthum:*
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6: em_estpl:*
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8: em_htc:*
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20: em_gss_vrt:*
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26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
	1	1069	26.0	3538	11	AK043210 Mus muscu
	2	797.8	19.4	865	9	AU118882 AU118882
	3	792.2	19.3	863	9	AU119546 AU119546
	4	789	19.2	869	9	AU120519 AU120519
	5	752.2	18.3	783	13	BX109539 BX109539
	6	750.6	18.3	3150	11	AK042211 Mus muscu
c	7	725.6	17.7	781	9	AI936539 wd29b09.x
	8	710.4	17.3	733	12	BM719244 UI-E-EO1-
c	9	704.2	17.2	777	12	BQ018994 UI-H-DH1-
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c	14	687.8	16.8	747	9	AI809396 wf70b01.x
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	41	554.4	13.5	578	13	BU948316 io49d10.y
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c	45	534.4	13.0	560	9	AU145859 AU145859

ALIGNMENTS

RESULT 1

AK043210

LOCUS AK043210 3538 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730071B21 product:SIMILAR TO ENDOTHELIN RECEPTOR TYPE A, full insert sequence.

ACCESSION AK043210

VERSION AK043210.1 GI:26335584

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3538)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
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Query Match 26.0%; Score 1069; DB 11; Length 3538;
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Matches 1501; Conservative 0; Mismatches 470; Indels 60; Gaps 9;

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Qy	500	CTCAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGTGATAATCCTGAGAGA	559
Db	325	CTTGCGGCATACTTTTGGCTGACCATGGTGGGAGGCGTAATGGCTGACAATCCGGAGAGA	384
Qy	560	TACAGCACAAATCTAAGCAATCATGTGGATGATTTACCACTTTTCGTGGCACAGAGCTC	619
Db	385	TACAGCGCTAATCTAAGCAGCCACATGGAAGACTTCACCCCTTTTCCGGGGACGGAGATC	444
Qy	620	AGCTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCTACCCAGCAATGGCTCAATG	679

Db	445	AACTTTCTGGGCACCAACCATCGACCCCTAATTTGGCCCTGCCTAGCAATGGCTCAATG	504
Qy	680	CACAACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTG	739
Db	505	CACGGCTATTGCCCACAGCAGACTAAAATCACGACAGCTTTCAAATATATTAACACTGTG	564
Qy	740	ATATCTTGTAATAATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATT	799
Db	565	ATATCCTGCACCAATTTTCATCGTGGGAATGGTGGGGAACGCAACTCTACTACGAATCATT	624
Qy	800	TACCAGAAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGA	859
Db	625	TACCAAAACAAGTGTATGAGGAACGGCCCCAATGCGCTCATAGCCAGCCTGGCCCTTGGA	684
Qy	860	GACCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGC	919
Db	685	GACCTTATCTACGTGGTCATTGACCTCCCATCAACGTGTTTAAGCTCTTGGCAGGACGC	744
Qy	920	TGGCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAG	979
Db	745	TGGCCTTTTCGACCACAATGATTTTGGAGTGTTTCTCTGCAAGCTGTTCCCTTCTCGAG	804
Qy	980	AAGTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGA	1039
Db	805	AAGTCCTCCGTGGGCATCACCGTCTTGAACCTCTGTGCTCTCAGTGTTGACAGGTACAGA	864
Qy	1040	GCAGTTGCCTCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAA	1099
Db	865	GCAGTGGCTTCCTGGAGCCGAGTTCAAGGAATCGGGATCCCCTTGATTACCGCCATTGAA	924
Qy	1100	ATTGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTTGAAGCGATTGGCTTCGTC	1159
Db	925	ATCGTCTCCATCTGGATTCTTTCCTTCATCTTGCCATCCCGGAAGCAATCGGCTTCGTC	984
Qy	1160	ATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCCACATCA	1219
Db	985	ATGGTACCCTTCGAATACAAGGGCGAGCTGCATAGGACCTGCATGCTCAACGCCACGTCC	1044
Qy	1220	AAATTTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGT	1279
Db	1045	AAGTTTCATGGAGTTTACCAAGATGTGAAGGACTGGTGGCTCTTGGGTTCTACTTCTGC	1104
Qy	1280	ATGCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGA	1339
Db	1105	ATGCCCTTGGTGTGCAAGCAATCTTCTACACCCTCATGACCTGTGAGATGCTCAACAGG	1164
Qy	1340	AGGAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCA	1399
Db	1165	AGGAACGGCAGCTTGGGATCGCCCTTAGTGAGCACCTCAAACAGCGTCGAGAAGTGGCA	1224
Qy	1400	AAAACAGTTTTCTGCTTGGTTGTAATTTTGCTCTTGTCTGGTTCCCTCTTCACTTAAGC	1459
Db	1225	AAGACTGTCTTCTGCTTGGTTGTATCTTCGCCCTGTGCTGGTTCCCTCTTCACTTAAGC	1284
Qy	1460	CGTATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCAGTGTGAATTACTTAGT	1519

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Db      1285 CGCATTTTGAAGAAAACGTATATGATGAGATGGATAAGAACCGGTGTGAACTGCTCAGC 1344
Qy      1520 TTCTTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAAC 1579
        ||||| ||||| ||||||||||||||| ||||| ||||||||||||||| || |||||||
Db      1345 TTCTTGCTGCTAATGGATTACATCGGCATTAACCTGGCAACCATGAATTCCTGCATAAAC 1404
Qy      1580 CCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGC 1639
        || ||||||| ||||||||||||||| ||||||||||| ||||| |||||||
Db      1405 CCAATAGCTCTATATTTTGTGAGCAAGAAATTCAAAAATTGTTTTCAGTCCTGCCTCTGT 1464
Qy      1640 TGCTGCTGTTACCAGTCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACAAGCATC 1699
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1465 TGCTGTTGTCAACAGTCCAAAAGCCTCATGACCTCGGTCCCATGAATGGAACGAGTATC 1524
Qy      1700 CAGTGGAAGAACCACGATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGC 1759
        ||||||||||||| || || ||||||||||||||| || ||||||||||| |||||||
Db      1525 CAGTGGAAGAACCAAGAGCAGAACAACCACAACACGGAACGGAGCAGCCACAAGGACAGC 1584
Qy      1760 ATGAACTGACCACCTTAGAAGCACTCCTCGGTACTCCCATATCCTCTCGGAGAAAAAA 1819
        ||||||| ||| || ||||| || || || || || || || || || || || || ||
Db      1585 ATGAACTAACCTCCGCAGAAACACCGAGACGTGTGCCTTCAAGTCTTAGGATGGAAACA 1644
Qy      1820 ATCACAAGGCAACTGTGACTCCGGAATCTCT-----TCTCTGATCCTTCTTCTTA 1871
        || || || || || || || || || || || || || || || || || || || ||
Db      1645 ACCATTACGCCACAGATGCGCTCCCAAACCTCCCAAGTCTCTCCCATGCTCCTTTTCTA 1704
Qy      1872 ATTCACTCCCAACCCCAAGAAGAAATGCTTTCCAAACCGCAAGGTAGACTGGTTTATCC 1931
        || || || || || || || || || || || || || || || || || || || ||
Db      1705 AGTCCATCCTAGGAAAAGCTCTCCTGCCCTCCCAACAGCACGTGGTGGACCGGT-----C 1759
Qy      1932 ACCCACAACATCTACGAATCGTACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTT 1991
        || || || || || || || || || || || || || || || || || || || ||
Db      1760 CCAGCTATAGCCAATGGGTCTTTCTGAGTACTGTATATGATTTCATACCGCGCATGTC 1819
Qy      1992 GTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCA 2051
        || || || || || || || || || || || || || || || || || || || ||
Db      1820 ATTTCCAACACTTGAAAAT-----TAGAGCTGGGAGAAAGGAGA-TGATGGTTCAAAGAA 1873
Qy      2052 GAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTAT 2111
        || || || || || || || || || || || || || || || || || || || ||
Db      1874 GCCACCTAGCTGCCGCCTTTGCATGAACACAGAGTTTGCAAGTTCATGACCAGCTTCCGT 1933
Qy      2112 GGCAGTTCTGGTGAATGTTCAATGGGAACTGGTCACCATGAACTTTAGAG 2162
        ||||||| || ||||||| || || || || || || || || || || || || ||
Db      1934 -GCAGTTCTATGGACCAGCTGGTGGGAACTGTCCATCCTAAGATTCTAGAG 1983

```

RESULT 2

AU118882

LOCUS AU118882 865 bp mRNA linear EST 01-AUG-2002

DEFINITION AU118882 HEMBA1 Homo sapiens cDNA clone HEMBA1004569 5', mRNA sequence.

ACCESSION AU118882

VERSION AU118882.1 GI:10934117

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 865)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished

COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES Location/Qualifiers

source 1. .865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1004569"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector: pME18SFL3"

BASE COUNT 271 a 184 c 158 g 247 t 5 others

ORIGIN

Query Match 19.4%; Score 797.8; DB 9; Length 865;
Best Local Similarity 98.0%; Pred. No. 6.1e-145;
Matches 847; Conservative 0; Mismatches 12; Indels 5; Gaps 4;

Qy 1479 TGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATT 1538
|| |||||

Db 1 TGNATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATT 60

Qy 1539 ACATCGGTATTAACTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTGTATTTTG 1598
|| |||||

Db 61 ACATCGGTATTAACTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTGTATTTTG 120

Qy 1599 TGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCA 1658
|| |||||

Db 121 TGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAGTCCA 180

Qy 1659 AAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAGTGGAAGAACCACGATC 1718
|| |||||

Db 181 AAAGTCTGATGACCTCGGTCCCCATGAACGGAACAAGCATCCAGTGGAAGAACCACGATC 240

Qy 1719 AAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAG 1778
|| |||||

Db 241 AAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCCTTAG 300

Qy 1779 AAGCACTCCTCGGTACTCCCATATCTCTCGGAGAAAAAATCACAAGGCAACTGTGAC 1838

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      |||
Db      301 AAGCACTCCTCGGTACTCCATAATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGAG 360
Qy      1839 TCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATG 1898
      |||
Db      361 TCCGGGAATCTCTTCTCTGATCCTTCTTCCTTAATTCACCTCCACACCCAAGAAGAAATG 420
Qy      1899 CTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTACGAATCGTACTT 1957
      |||
Db      421 CTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACATCTACGAATCGTACTT 480
Qy      1958 CTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTAGCACTAAAAAATGGTGGGA 2017
      |||
Db      481 CTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTAGCACTAAAAAATGGTGGGA 540
Qy      2018 GCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGCATGA 2077
      |||
Db      541 GCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGCATGA 600
Qy      2078 AAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGG 2137
      |||
Db      601 AAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAATGGG 660
Qy      2138 AACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA- 2196
      |||
Db      661 AACTGGTCACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAGTGA 720
Qy      2197 TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATT 2256
      |||
Db      721 TTTTTTGNCTTCAGCCAAACACAATATGGGCTCAAGTCACTTTTATTTGAAATGNCATT 780
Qy      2257 TGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATG--ATTATTTGAACTTATTTA- 2313
      |||
Db      781 TGGTGCCAGTATTTTTTAACTGCATAATAGCCTAACATGGATTATTTGGAACCTTATTTAC 840
Qy      2314 CACATAGTTTGAAAAAAAAAAGAC 2337
      |||
Db      841 CNCNTAGTTTGAAAAAAAAAAGAC 864

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RESULT 3

AU119546

LOCUS AU119546 863 bp mRNA linear EST 01-AUG-2002

DEFINITION AU119546 HEMBA1 Homo sapiens cDNA clone HEMBA1006071 5', mRNA sequence.

ACCESSION AU119546

VERSION AU119546.1 GI:10934781

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 863)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

Qy	2463	TGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAAT	2522
Db	420	TGGCAGTTTAAATAGATGTTACTCAAAGAATTTTTTAAGAACTGTATTTTATTTTTTAAAT	479
Qy	2523	GGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTT	2582
Db	480	GGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATGTTAAATTCAAAGTAATGCTT	539
Qy	2583	CAATCAGATAGTTCTTTTTTCAAGTTCAATACTGTTTTTCATGTAAATTTTGTATGAAA	2642
Db	540	CAATCAGATAGTTCTTTTTTCAAGTTCAAT-CTGTTTTTCATGTAAATTTTGTATGAAA	598
Qy	2643	AATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTC	2702
Db	599	AATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCATTTAACTCTGCCTGAGACTTTC	658
Qy	2703	AGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGAT	2762
Db	659	AGTGCACCTGTATATAGAAGTCTAAAACACACCTAAGAGAAAAAGATCGAATTTTTCAGAT	718
Qy	2763	GATTTCGGAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGTATATACATATCA	2822
Db	719	GATTTCGGAATTTTCATTCAAGTATTTGTAATAGTGACATATATATGNATATACATATCA	778
Qy	2823	CCTCCTATTCTCTTAATTTTGTAAAAATGTTAACTGGCAGT-AAGTCTTTTTTGATCAT	2881
Db	779	CCTCCTATTCTCTTAATTTTCTTAAAAATGGTAACTGGCAGTAAAGCCTTTTTTGACCAT	838
Qy	2882	TCCCTTTTCCATATAGGAAACATA	2905
Db	839	TCCCTTTTCATTTAGGGAAACTTA	862

RESULT 4

AU120519

LOCUS AU120519 869 bp mRNA linear EST 01-AUG-2002

DEFINITION AU120519 HEMBB1 Homo sapiens cDNA clone HEMBB1000846 5', mRNA sequence.

ACCESSION AU120519

VERSION AU120519.1 GI:10935754

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 869)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished

COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986

Qy 2309 ATTTACACATAGTTTGAAGAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATTAGATTA 2368
 |||
 Db 541 ATTTACACATAGTTTGAAGAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATTAGATTA 600

Qy 2369 GTATTTTCCACGTCACTATTTATTTTAAAAACACAAATTCTAAAGCTACAACAAATAC 2428
 |||
 Db 601 GTATTTTCCACGTCACTGGTTATTTTAAAAACACANATTCTAAAGCTACAACAAATAC 660

Qy 2429 TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAA 2488
 |||
 Db 661 TACAGGCCCTTAAAGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAA 720

Qy 2489 GAATTTTAAAGAACTGTATTTTATTTTAAATGGTGTATTATTACAAGGGACCTTGAA 2548
 |||
 Db 721 GAATTTTAAAGAACTGNATTTTATTTTGAATGGTGTATTATTACAAGGGACCTTG-A 779

Qy 2549 CATGTTTTGTATGTTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTCACAAGT 2608
 |||
 Db 780 CATGTTTTGGATGGTAAATTCAAAGTAATGCTTCAATCAGATAGTTC-TTTTTCACAAGT 838

Qy 2609 TCAATACTGTTTTTCATGTAAATTTTG 2635
 |||
 Db 839 TCAAT-CTGGTTTTTCATGTAAATTTGG 864

RESULT 5

BX109539

LOCUS BX109539 783 bp mRNA linear EST 07-FEB-2003

DEFINITION BX109539 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
 IMAGp998G221159 ; IMAGE:487341, mRNA sequence.

ACCESSION BX109539

VERSION BX109539.1 GI:27877774

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 783)

AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
 Radelof,U., Schneider,D. and Korn,B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGp998G221159.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human UnigeneSet - RZPD3 (RZPDLIB No.972)

[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)

[bin/showLib.pl.cgi/response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972) Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;


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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      418 GTGATTGTTTCATCATGACAACCTGCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCAT 477
Qy      3379 TCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCA 3438
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      478 TCATAAATCTTGTAATCATGTTACCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCA 537
Qy      3439 GATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTA 3498
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      538 GATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTA 597
Qy      3499 TTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATAT 3558
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      598 TTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTTGAAGTATTATAT 657
Qy      3559 TGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCA 3618
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      658 TGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCA 717
Qy      3619 GACTTCGCCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTTGTTGGGCCATATTT 3678
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      718 GACTTCGCCCAGACAGATTGCTGATAATAAATTANGTAAGATAATTTGNTGGGCCATATTT 777
Qy      3679 TAGGAC 3684
      || |||
Db      778 TANGAC 783

```

RESULT 6

AK042211

LOCUS AK042211 3150 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630071G03 product:SIMILAR TO ENDOTHELIN RECEPTOR TYPE A, full insert sequence.

ACCESSION AK042211

VERSION AK042211.1 GI:26088888

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3150)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

Qy	322	CCCTCCGCGCCACCCACCTCGCTTTCTCCGGCTTCTCTGCGCCAGGCGCCGCGGGAC	381
Db	286	CCCTGCGCGCCACCCTCGTTCTCCAGCTCAGGCTCCGGCTGGCCCGTGCGC-----GGA	339
Qy	382	CCGGCAGCTGTCTGCGCACGCCGAGCTCCACGGTGAAAAAAAAAAGTGAAGGTGTAAAAGC	441
Db	340	CCTGGAGCTGTCTGCTTCCGAGGAGCTCTAAGGTGAAAAAAGAAAGGCGTGAGACCAAC	399
Qy	442	AGCACAAAGTGCAATAAGAGATATTTCTCAAATTTGCCTCAAGATGGAAACCCTTTGCCT	501
Db	400	ATAAGAAG-----ACTTAAATCCAGGTTAAGATGAGTATCTTTTGCCT	443
Qy	502	CAGGGCATCCTTTTGGCTGGCACTGGTTGGATGTGTAATCAGTGATAATCCTGAGAGATA	561
Db	444	TGCGGCATACTTTTGGCTGACCATGGTGGGAGGCGTAATGGCTGACAATCCGGAGAGATA	503
Qy	562	CAGCACAAATCTAAGCAATCATGTGGATGATTTCAACCACTTTTCGTGGCACAGAGCTCAG	621
Db	504	CAGCGCTAATCTAAGCAGCCACATGGAAGACTTCAACCCCTTTTCCGGGGACGGAGATCAA	563
Qy	622	CTTCCTGGTTACCACTCATCAACCCACTAATTTGGTCCTACCCAGCAATGGCTCAATGCA	681
Db	564	CTTTCTGGGCACCACCCATCGACCCCTAATTTGGCCCTGCCTAGCAATGGCTCAATGCA	623
Qy	682	CAACTATTGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGAT	741
Db	624	CGGCTATTGCCCACAGCAGACTAAAATCACGACAGCTTTCAAATATATTAACACTGTGAT	683
Qy	742	ATCTTGTAATAATTTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTA	801
Db	684	ATCCTGCACCAATTTTTCATCGTGGGAATGGTGGGGAACGCAACTCTACTACGAATCATTTA	743
Qy	802	CCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGA	861
Db	744	CCAAAACAAGTGATGAGGAACGGCCCCAATGCGCTCATAGCCAGCCTGGCCCTTGGAGA	803
Qy	862	CCTTATCTATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTG	921
Db	804	CCTTATCTACGTGGTCATTGACCTCCCCATCAACGTGTTTAAGCTCTTGGCAGGACGCTG	863
Qy	922	GCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTCGAGAA	981
Db	864	GCCTTTTCGACCACAATGATTTTGGAGTGTTTCTCTGCAAGCTGTTCCCTTCTGCAGAA	923
Qy	982	GTCCTCGGTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGC	1041
Db	924	GTCCTCCGTGGGCATCACCGTCTTGAACCTCTGTGCTCTCAGTGTGGACAGGTACAGAGC	983
Qy	1042	AGTTGCCTCCTGGAGTCGTGTTTCAAGGAATTGGGATTCTTTGGTAACTGCCATTGAAAT	1101
Db	984	AGTGGCTTCTCGGAGCCGAGTTCAAGGAATCGGGATCCCCTTGATTACCGCCATTGAAAT	1043
Qy	1102	TGTCTCCATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCTAT	1161
Db	1044	CGTCTCCATCTGGATTCTTTCTTTCATCTTGGCCATCCCGGAAGCAATCGGCTTCGTCTAT	1103

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Qy      1162 GGTACCCTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCCACATCAA 1221
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1104 GGTACCCTTCGAATACAAGGGCGAGCTGCATAGGACCTGCATGCTCAACGCCACGTCCAA 1163

Qy      1222 ATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTAT 1281
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1164 GTTCATGGAGTTTACCAAGATGTGAAGGACTGGTGGCTCTTTGGGTTCTACTTCTGCAT 1223

Qy      1282 GCCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAG 1341
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1224 GCCCTTGGTGTGCACAGCAATCTTCTACACCCTCATGACCTGTGAGATGCTCAACAGGAG 1283

Qy      1342 GAATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAG 1384
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1284 GAACGGCAGCTTGCGGATCGCCCTTAGTGAGCACCTCAAACAG 1326

```

RESULT 7

AI936539/c

LOCUS AI936539 781 bp mRNA linear EST 17-DEC-1999

DEFINITION wd29b09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:2329529 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR
 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI936539

VERSION AI936539.1 GI:5675409

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 781)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1132 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 456.

FEATURES

source

Location/Qualifiers

1. .781

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2329529"

/lab_host="DH10B"

/clone_lib="Soares_NFL_T_GBC_S1"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NbHL19W, testis NHT, and B-cell
 NCI_CGAP_GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver


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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      114 CTACCTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCC 55

Qy      4056 CTGAGTTGGCAGTGGCCCATAGTGTAATAAAAGTTTACAGAAACCTT 4105
      ||||||||||||||||||||||||||||||||||||||||||||| || || || ||
Db      54 CTGAGTTGGCAGTGGCCCATAGTGTAATAAAAGTTAACAAAACCTT 5

```

RESULT 8

BM719244

LOCUS BM719244 733 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-EO1-ajd-b-04-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-ajd-b-04-0-UI 5', mRNA sequence.

ACCESSION BM719244

VERSION BM719244.1 GI:19037818

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 733)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1. .733

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-EO1-ajd-b-04-0-UI"

/tissue_type="fetal eye"

/dev_stage="fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-EO1"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EO1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 199 a 115 c 150 g 267 t 2 others
ORIGIN

Query Match 17.3%; Score 710.4; DB 12; Length 733;
Best Local Similarity 99.4%; Pred. No. 6.7e-128;
Matches 722; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy	3162	TGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTG	3221
Db	1	TGTAAATTTCTTTTAGCCCATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTGTG	60
Qy	3222	ATATATGCATGTGTGTGATGGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGC	3281
Db	61	ATATATGCATGTGTGTGATGGTATGTATGGATTTAATCTAATCTAATAATTGTGCCCCGC	120
Qy	3282	AGTTGTGCCAAAGTGCATAGTCTGAGCTAAAATCTAGGTGATTGTTTCATCATGACAACCT	3341
Db	121	AGTTGTGCCAAAGTGCATAGTCTGAG-TAAAATCTAGGTGATTGTTTCATCATGACAACCT	179
Qy	3342	GCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTA	3401
Db	180	GCCTCAGTCCATTTTAACCTGTAGCAACCTTCTGCATTCATAAATCTTGTAATCATGTTA	239
Qy	3402	CCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATAT	3461
Db	240	CCATTACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATAT	299
Qy	3462	AGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGT	3521
Db	300	AGGGTTTTGTTTGGTTGGTTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGT	359
Qy	3522	GCTGGAGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGT	3581
Db	360	GCTGGAGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGT	419
Qy	3582	GGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGA	3641
Db	420	GGTGATGAAATTGCCAGGTTGTCTGATATTTCTTTCAGACTTCGCCAGACAGATTGCTGA	479
Qy	3642	TAATAAATTAGGTAAGATAAATTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAG	3701
Db	480	TAATAAATTAGGTAAGATAAATTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAG	539
Qy	3702	GTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAA	3761
Db	540	GTTCCAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAN	599

Qy 3762 ATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGG 3821
 |||
 Db 600 ATCTATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGG 659

Qy 3822 TTCACACCATTTTGTGTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATG 3881
 |||
 Db 660 TTCACACCATTTTGTGTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATG 719

Qy 3882 AAAAAA 3887
 ||||
 Db 720 NAAAAA 725

RESULT 9

BQ018994/c

LOCUS BQ018994 777 bp mRNA linear EST 27-MAR-2002

DEFINITION UI-H-DH1-awv-o-07-0-UI.s1 NCI_CGAP_DH1 Homo sapiens cDNA clone
 IMAGE:5824350 3', mRNA sequence.

ACCESSION BQ018994

VERSION BQ018994.1 GI:19754271

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 777)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..777

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5824350"

/tissue_type="Metastatic Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_DH1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;

NCI_CGAP_DH1 is a normalized cDNA library containing the
 following tissue(s): VS-8 Cell line from Metastatic

Chondrosarcoma in Lung. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC.

TAG_LIB=UI-H-DH1

TAG_TISSUE=lung

TAG_SEQ=AGATCATTGC"

BASE COUNT 219 a 138 c 166 g 253 t 1 others
ORIGIN

Query Match 17.2%; Score 704.2; DB 12; Length 777;
Best Local Similarity 97.9%; Pred. No. 1.1e-126;
Matches 734; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Qy      1595 TTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAG 1654
          |||||      |||||
Db      750 TATNTGTGAGCAAGAATTTAAAAATGTTTCCAGTCATGCCTCTGCTGCTGCTGTTACCAG 691

Qy      1655 TCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACAAGCATCCAGTGAAGAACCAC 1714
          |||||
Db      690 TCCAAAAGTCTGATGACCTCGGTCCCATGAACGGAACAAGCATCCAGTGAAGAACCAC 631

Qy      1715 GATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCC 1774
          |||||
Db      630 GATCAAAACAACCACAACACAGACCGGAGCAGCCATAAGGACAGCATGAACTGACCACCC 571

Qy      1775 TTAGAAGCACTCCTCGGTACTCCCATATCTCTCGGAGAAAAAATCACAAGGCAACTG 1834
          |||||
Db      570 TTAGAAGCACTCCTCGGTACTCCCATATCTCTCGGAGAAAAAATCACAAGGCAACTG 511

Qy      1835 TGACTCCGGGAATCTCTTCTCTGATCCTTCTTCTTAATTCACTCCCAACCCAAGAAGA 1894
          |||
Db      510 TGAGTCCGGGAATCTCTTCTCTGATCCTTCTTCTTAATTCACTCCCAACCCAAGAAGA 451

Qy      1895 AATGCTTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTACGAATCGT 1953
          |||||
Db      450 AATGCTTTTCCAAAACCGCAAGGGTAGACTGGTTTATCCACCCACAACATCTACGAATCGT 391

Qy      1954 ACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGT 2013
          |||||
Db      390 ACTTCTTTAATTGATCTAATTTACATATTCTGCGTGTTGTATTTCAGCACTAAAAAATGGT 331

Qy      2014 GGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGC 2073
          |||||
Db      330 GGGAGCTGGGGGAGAATGAAGACTGTTAAATGAAACCAGAAGGATATTTACTACTTTTGC 271

Qy      2074 ATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAA 2133
          |||||
Db      270 ATGAAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGGTGAATGTTCAA 211

Qy      2134 TGGGAACTGGTCAACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAG 2193
          |||||
Db      210 TGGGAACTGGTCAACCATGAAACTTTAGAGATTAACGACAAGATTTTCTACTTTTTTTAAG 151

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Qy      2194 TGA-TTTTTTGTCTTCAGCCAAACACAATATGGGCTCAGGTCACTTTTATTTGAAATGT 2252
      ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      150 TGATTTTTTTGTCTTCAGCCAAACACAATATGGGCTCAAGTCACTTTTATTTGAAATGT 91

Qy      2253 CATTTGGTGCCAGTATTTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTTATTT 2312
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90  CATTTGGTGCCAGTATTTTTTTAACTGCATAATAGCCTAACATGATTATTTGAACTTATTT 31

Qy      2313 ACACATAGTTTGAAAAAAAAAAGACAAAAA 2342
      ||||||||||||||||||||||||||||
Db      30  ACACATAGTTTGAAAAAAAAAAGACAAAAA 1

```

RESULT 10

AU139639

LOCUS AU139639 764 bp mRNA linear EST 05-AUG-2002

DEFINITION AU139639 PLACE1 Homo sapiens cDNA clone PLACE1011029 5', mRNA sequence.

ACCESSION AU139639

VERSION AU139639.1 GI:11001160

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 764)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES Location/Qualifiers

source

1. .764

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PLACE1011029"

/tissue_type="placenta"

/clone_lib="PLACE1"

/note="Vector: pME18SFL3"

BASE COUNT 252 a 134 c 111 g 263 t 4 others

ORIGIN

Query Match 17.0%; Score 695.8; DB 9; Length 764;

Best Local Similarity 97.6%; Pred. No. 4.7e-125;

Matches 726; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

Qy	2322	TTGAAAAAAAAAAGACAAAAATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGT	2381
Db	5	TTTGAAAAAAAAAAGACAAAAATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGT	64
Qy	2382	CACTATTTATTTTTTTTAAAAACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAA	2441
Db	65	CACTGTTTATTTTTTTTAAAAACACAAATTCTAAAGCTACAACAAATACTACAGGCCCTTAA	124
Qy	2442	AGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGA	2501
Db	125	AGCACAGTCTGATGACACATTTGGCAGTTTAATAGATGTTACTCAAAGAATTTTTTAAGA	184
Qy	2502	ACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATG	2561
Db	185	ACTGTATTTTATTTTTTAAATGGTGTTTTATTACAAGGGACCTTGAACATGTTTTGTATG	244
Qy	2562	TTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTTACAAGTTCAATACTGTTTT	2621
Db	245	TTAAATTCAAAGTAATGCTTCAATCAGATAGTTCTTTTTTACAAGTTCAAT-CTGTTTT	303
Qy	2622	TCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAT	2681
Db	304	TCATGTAAATTTTGTATGAAAAATCAATGTCAAGTACCAAATGTTAATGTATGTGTCAT	363
Qy	2682	TTAACTCTGCCTGAGACTTTCAGTGCACGTGTATATAGAAGTCTAAAACACACCTAAGAGA	2741
Db	364	TTAACTCTGCCTGAGACTTTCAGTGCACGTGTATATAGAAGTCTACAACACACCTAAGAGA	423
Qy	2742	AAAAGATCGAATTTTTTCAGATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACA	2801
Db	424	AAAAGATCGAATTTTTTCAGATGATTCAGAAATTTTCATTCAGGTATTTGTAATAGTGACA	483
Qy	2802	TATATATGTATATACATATCACCTCCTATTCTCTTAATTTTTTGTAAATGTAACTGGC	2861
Db	484	TATATATGTATATACATATCACCTCCTATTCTCTTAATTTTTTCTTAAATGTAACTGGC	543
Qy	2862	AGTAAGTCTTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAG	2921
Db	544	AGTAAGTCTTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGNCAG	603
Qy	2922	ATGAGTTTATCATGTGTCAGTGAAAAATAATTACCCACAAATGCCACCAGTAACTTAACGAT	2981
Db	604	ATGAGTTTATCATGTGTCAGTGAAAAATAATTACCCACAAATGCCACCAG--AACTTACGAT	661
Qy	2982	TCTTCACTTCTTGGGGTTTTTTCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA	3041
Db	662	TCCTCACTTCTTGGGGTTTTTTCAGTATGAACCTAACTCCCCACCCCAACATCTCCCTCCCA	721
Qy	3042	CATTGTCACCATTTCAAAGGGCCC	3065
Db	722	CATTGGCACCANTTCAAAGGGGNC	745

RESULT 11

CD246193

LOCUS

CD246193

782 bp

mRNA

linear

EST 22-MAY-2003

[illegible]

RESULT 12
AI694278/c


```

      |||
Db      441 GCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGCTAA 382
      |||
Qy      3730 GAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATG 3789
      |||
Db      381 GAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCATATG 322
      |||
Qy      3790 CAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATTGTC 3849
      |||
Db      321 CAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATTGTC 262
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Qy      3850 TTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 3909
      |||
Db      261 TTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 202
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Qy      3910 GTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAGTGTGG 3969
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Db      201 GTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAAGTGTGG 142
      |||
Qy      3970 TTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACTTT 4029
      |||
Db      141 TTTACTAGCAGGACTATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAACTTT 82
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Qy      4030 GTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAAAATAAA 4089
      |||
Db      81 GTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAGTGTAAAATAAA 22
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Qy      4090 AGTTTACAGAAACCTT 4105
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Db      21 AGTTTACAGAAACCTT 6

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RESULT 13

BQ575745/c

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LOCUS      BQ575745          732 bp    mRNA    linear    EST 19-JUN-2002
DEFINITION UI-H-EZ1-bbg-h-22-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
            UI-H-EZ1-bbg-h-22-0-UI 3', mRNA sequence.
ACCESSION  BQ575745
VERSION    BQ575745.1  GI:21479062
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 732)
  AUTHORS  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL  Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthopaedics
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained

```

from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES
source Location/Qualifiers
1. .732
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZ1-bbg-h-22-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ch2"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCACGCT.
TAG_LIB=UI-H-EZ1
TAG_TISSUE=grade-2-chondrosarcoma
TAG_SEQ=ATCTAATATG"

BASE COUNT 242 a 146 c 110 g 231 t 3 others
ORIGIN

Query Match 16.9%; Score 692.2; DB 13; Length 732;
Best Local Similarity 99.1%; Pred. No. 2.4e-124;
Matches 694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3406 TACAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGG 3465
|| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 718 TANCAAATGGGATATAAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGG 659

Qy 3466 TTTTGTGGTTGGTTGGTTGGTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTG 3525
|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db 658 TTTTGTGGTTGGTTGGTTGGTNTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTG 599

Qy 3526 GAGCAAAAGTCATTACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTG 3585
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Db 598 GAGCAAAAGTCATTACACTNTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTG 539

Qy 3586 ATGAAATTGCCAGGTTGTCTGATATTTCTTTGAGCTTCGCCAGACAGATTGCTGATAAT 3645
|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db 538 ATGAAATTGCCAGGTTGTCTGATATTTCTTTGAGCTTCGCCAGACAGATTGCTGATAAT 479

Qy 3646 AAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTTC 3705
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Db 478 AAATTAGGTAAGATAATTTGTTGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTTC 419

Qy 3706 CAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCT 3765
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 Db 418 CAGTTGCTTGAATTGCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCT 359

Qy 3766 ATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCA 3825
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 Db 358 ATTATTCCACTGGCGCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTCA 299

Qy 3826 CACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAA 3885
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 Db 298 CACCATTTTGTTTAGACAATTGTCTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAA 239

Qy 3886 AAATGCATTTTATAAATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTAT 3945
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 Db 238 AAATGCATTTTATAAATTGAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTAT 179

Qy 3946 TTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTAC 4005
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 Db 178 TTATGGACTGGTAAGTAACTGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTAC 119

Qy 4006 TACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGC 4065
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 Db 118 TACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGC 59

Qy 4066 AGTGGCCCATAGTGTAAAATAAAAGTTTACAGAAACCTT 4105
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 Db 58 AGTGGCCCATAGTGTAAAATAAAAGTTTACAGAAACCTT 19

RESULT 14

AI809396/c

LOCUS AI809396 747 bp mRNA linear EST 19-DEC-1999
 DEFINITION wf70b01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:2360905 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR
 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI809396
 VERSION AI809396.1 GI:5395962
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 747)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1717 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 466.

FEATURES Location/Qualifiers
 source 1..747
 /organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2360905"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

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BASE COUNT      250 a      154 c      118 g      221 t      4 others
ORIGIN

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Query Match          16.8%; Score 687.8; DB 9; Length 747;
Best Local Similarity 98.1%; Pred. No. 1.7e-123;
Matches 725; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

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Qy      3368 ACCTTCTGCATTTCATAAATCTTGTAAATCATGTTACCATTACAAATGGGATATAAGAGGCCA 3427
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Db      742 ACCTTCTGCATTTCAT-AATCTGGTAATCATG-TACCATACNNAATGGGATATAAGAGGCCA 685

Qy      3428 GCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGG-TTGGTTT 3486
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      684 GCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTGGGTTTGGTNT 625

Qy      3487 GATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTT 3546
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      624 GATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATTACACTTT 565

Qy      3547 GAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGTCTG 3606
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      564 GAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGGTTGGTCTG 505

Qy      3607 ATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTTGT 3666
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Db      504 ATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGATAATTTGT 445

Qy      3667 TGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGC 3726
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Db      444 TGGGCCATATTTTAGGACAGGTAAAATAACATCAGGTTCCAGTTGCTTGAATTGCAAGGC 385

Qy      3727 TAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCAT 3786
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Db      384 TAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGCGCATCAT 325

Qy      3787 ATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATT 3846
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      324 ATGCAGTGATATATGCCCTATAATATAAGCCATAGGTTACACCATTTTGTTTAGACAATT 265

Qy      3847 GTCTTTTTTTTCAAGATGCTTTTGTCTTTTCATATGAAAAAATGCATTTTATAAATTCAG 3906

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Db      264 GTCTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATAAATTCAG 205
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Qy      3907 AAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAACTG 3966
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Qy      3967 TGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAAC 4026
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Db      144 TGGTTTACTAGCAGGACTATTTCCAATTTCTACCTTTACTACATCTTTTCAACAAGTAAC 85
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Qy      4027 TTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAATAAT 4086
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Db      84 TTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAATAAT 25
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Qy      4087 AAAAGTTTACAGAAACCTT 4105
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Db      24 AAAAGTTTACAGAAACCTT 6

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RESULT 15

BQ006584/c

LOCUS BQ006584 705 bp mRNA linear EST 26-MAR-2002

DEFINITION UI-H-EI1-aza-f-14-0-UI.s1 NCI_CGAP_EI1 Homo sapiens cDNA clone
IMAGE:5846029 3', mRNA sequence.

ACCESSION BQ006584

VERSION BQ006584.1 GI:19731484

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 705)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES Location/Qualifiers

source

1. .705

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5846029"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_EI1"

/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_EI1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTTGAC.

TAG_LIB=UI-H-EI1

TAG_TISSUE=chondrosarcoma

TAG_SEQ=ACACTTGAC"

BASE COUNT 235 a 143 c 106 g 220 t 1 others
ORIGIN

Query Match 16.7%; Score 685; DB 12; Length 705;
Best Local Similarity 99.9%; Pred. No. 6e-123;
Matches 685; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      705 AAGAGGCAGCGTGAAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTTTGGTTGG 646

Qy      3480 TTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATT 3539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      645 TTGGTTTGATAAAGCAGTATTTGGGGTCATATTGTTTCCTGTGCTGGAGCAAAAGTCATT 586

Qy      3540 ACACTTTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGG 3599
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      585 ACACTNTGAAGTATTATATTGTTCTTATCCTCAATTCAATGTGGTGATGAAATTGCCAGG 526

Qy      3600 TTGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGAT 3659
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Db      525 TTGTCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGATAATAAATTAGGTAAGAT 466

Qy      3660 AATTTGTTGGGCCATATTTTAGGACAGGTAAATAACATCAGGTTCCAGTTGCTTGAATT 3719
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Db      465 AATTTGTTGGGCCATATTTTAGGACAGGTAAATAACATCAGGTTCCAGTTGCTTGAATT 406

Qy      3720 GCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGC 3779
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Db      405 GCAAGGCTAAGAAGTACTGCCCTTTTGTGTGTTAGCAGTCAAATCTATTATTCCACTGGC 346

Qy      3780 GCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTA 3839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      345 GCATCATATGCAGTGATATATGCCTATAATATAAGCCATAGGTTACACCATTTTGTTTA 286

Qy      3840 GACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATA 3899
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Db      285 GACAATTGTCTTTTTTTTCAAGATGCTTTGTTTCTTTTCATATGAAAAAATGCATTTTATA 226

Qy      3900 AATTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAA 3959
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Db      225  |||||AATTTCAGAAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAA 166
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Db      165  |||||GTAACGTGGTTTACTAGCAGGAATATTTCCAATTTCTACCTTTACTACATCTTTTCAAC 106
Qy      4020 AAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGT 4079
Db      105  |||||AAGTAACTTTGTAGAAATGAGCCAGAAGCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGT 46
Qy      4080 GTAAAATAAAAGTTTACAGAAACCTT 4105
Db      45   |||||GTAAAATAAAAGTTTACAGAAACCTT 20

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Search completed: December 12, 2003, 23:51:38
Job time : 7408.45 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:18:36 ; Search time 258.387 Seconds
(without alignments)
7347.063 Million cell updates/sec

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Perfect score: 4301
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4301	100.0	4301	4 US-08-121-446-3	Sequence 3, Appli
2	1691.8	39.3	1873	3 US-08-910-864-13	Sequence 13, Appl
3	1466.8	34.1	1470	4 US-09-016-434-1203	Sequence 1203, Ap
4	1070.4	24.9	1321	4 US-09-175-658B-20	Sequence 20, Appl
5	395.8	9.2	4079	4 US-09-016-434-1257	Sequence 1257, Ap
6	395.8	9.2	4105	4 US-08-121-446-1	Sequence 1, Appli
7	132.2	3.1	1700	5 PCT-US92-02091-1	Sequence 1, Appli
8	114.6	2.7	246240	2 US-08-724-394A-20	Sequence 20, Appl
9	114.6	2.7	246240	2 US-08-724-394A-21	Sequence 21, Appl
10	114.6	2.7	246240	2 US-08-724-394A-22	Sequence 22, Appl
11	108.8	2.5	1584	5 PCT-US92-02091-5	Sequence 5, Appli

c	12	107.2	2.5	801	4	US-09-175-658B-25	Sequence 25, Appl
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	14	106.6	2.5	1413	4	US-09-016-434-1275	Sequence 1275, Ap
	15	106	2.5	1726	4	US-09-016-434-1215	Sequence 1215, Ap
	16	106	2.5	1726	5	PCT-US92-02091-3	Sequence 3, Appli
	17	101.6	2.4	1352	4	US-09-016-434-1233	Sequence 1233, Ap
	18	101.6	2.4	1352	5	PCT-US92-02091-7	Sequence 7, Appli
	19	98.6	2.3	1563	1	US-08-279-590A-1	Sequence 1, Appli
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	21	89.6	2.1	259	4	US-09-016-434-921	Sequence 921, App
	22	88	2.0	1842	4	US-09-170-496D-91	Sequence 91, Appl
	23	88	2.0	1842	4	US-09-170-496D-211	Sequence 211, App
	24	88	2.0	4953	4	US-09-620-312D-240	Sequence 240, App
	25	84.8	2.0	4156	1	US-08-465-687A-1	Sequence 1, Appli
	26	84.8	2.0	4156	3	US-09-030-970-1	Sequence 1, Appli
	27	84.8	2.0	4156	4	US-09-520-210-1	Sequence 1, Appli
	28	84.8	2.0	4156	5	PCT-US94-11843-1	Sequence 1, Appli
	29	80.6	1.9	1443	3	US-08-959-381A-3	Sequence 3, Appli
	30	80.6	1.9	1446	4	US-09-170-496D-81	Sequence 81, Appl
	31	80.6	1.9	1446	4	US-09-170-496D-207	Sequence 207, App
	32	80.6	1.9	1626	3	US-08-959-381A-4	Sequence 4, Appli
c	33	63.4	1.5	20674	4	US-09-641-638-651	Sequence 651, App
	34	63.2	1.5	595	1	US-08-784-289-1	Sequence 1, Appli
	35	61.8	1.4	1605	4	US-09-676-970-1	Sequence 1, Appli
	36	61.8	1.4	1605	4	US-09-676-972B-1	Sequence 1, Appli
	37	61.8	1.4	1605	4	US-09-016-434-1231	Sequence 1231, Ap
	38	61.8	1.4	1605	4	US-09-676-941A-1	Sequence 1, Appli
	39	61.8	1.4	1605	4	US-10-013-846-3	Sequence 3, Appli
	40	61.8	1.4	2624	1	US-08-232-144-3	Sequence 3, Appli
	41	61.8	1.4	4571	1	US-08-232-144-5	Sequence 5, Appli
	42	60.8	1.4	511	4	US-09-175-658B-22	Sequence 22, Appl
c	43	60.6	1.4	1864	4	US-09-468-265-4	Sequence 4, Appli
	44	60.2	1.4	1152	3	US-09-045-186-1	Sequence 1, Appli
	45	60.2	1.4	1152	3	US-09-045-186-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-121-446-3

; Sequence 3, Application US/08121446

; Patent No. 6313276

; GENERAL INFORMATION:

; APPLICANT: IMURA, HIROO

; APPLICANT: NAKAO, KAZUWA

; APPLICANT: NAKANISHI, SHIGETADA

; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1566
US-08-121-446-3

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Query Match          100.0%; Score 4301; DB 4; Length 4301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
        |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        |||
Db     61 AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        |||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

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Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200

Qy 1201 GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260
 |||
 Db 1201 GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260

Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAAC'TTTTG 1320
 |||
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAAC'TTTTG 1320

Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380
 |||
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

Qy 1381 AACC'CAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC'TGCTTTAAGTCATGCTTA 1440
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 Db 1381 AACC'CAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC'TGCTTTAAGTCATGCTTA 1440

Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500
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 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500

Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560
 |||
 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560

Qy 1561 TCTTGAAAGAAGAACTATTC'ACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA 1620
 |||
 Db 1561 TCTTGAAAGAAGAACTATTC'ACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA 1620

Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680
 |||
 Db 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680

Qy 1681 TAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT 1740
 |||
 Db 1681 TAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT 1740

Qy 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800
 |||
 Db 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800

Qy 1801 TTTT'TACAGTTAGCACTTCAACATAGCTCTTAACAAC'TCCAGGATATTCACACAACACT 1860
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 Db 1801 TTTT'TACAGTTAGCACTTCAACATAGCTCTTAACAAC'TCCAGGATATTCACACAACACT 1860

Qy 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTA 1920
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 Db 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTA 1920

Qy 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG 1980
 |||
 Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG 1980

Qy 1981 AAGCTTAAATTA'CTCAATTTAAAATTTTAAAATCCTTTAAAACAAC'TTTTCAATTAATAT 2040
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 Db 1981 AAGCTTAAATTA'CTCAATTTAAAATTTTAAAATCCTTTAAAACAAC'TTTTCAATTAATAT 2040

Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100

Db	2041	 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTGTGTCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	 TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCGTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCGTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940

Db	2881	AGCTTTGTGCGTTCCCTGCCCTAATTTTATATCTTCTAAGCAAAGTGCCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAAATGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAAATGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840
 ||||||||||||||||||
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTATATAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
 ||||||||||||||||||
 Db 3841 CAGCTCAAAGATTATATAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
 ||||||||||||||||||
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
 ||||||||||||||||||
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
 ||||||||||||||||||
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
 ||||||||||||||||||
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200
 ||||||||||||||||||
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
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 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301

RESULT 2

US-08-910-864-13

; Sequence 13, Application US/08910864

; Patent No. 6280931

; GENERAL INFORMATION:

; APPLICANT: SAKAMOTO, AIJI

; APPLICANT: HANAOKA, FUMIO

; TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A cDNA OF AN
 EXTREMELY

; TITLE OF INVENTION: SMALL QUANTITY

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & RICHARDSON P.C.

; STREET: 4225 EXECUTIVE SQUARE, SUITE 1400

; CITY: LA JOLLA

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,864
; FILING DATE: 13-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 216506/1996
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07898/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1556
US-08-910-864-13

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Query Match 39.3%; Score 1691.8; DB 3; Length 1873;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	178	TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC	237
Db	171	TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC	230
Qy	238	ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC	297
Db	231	ATGCAGCCGCCTCCAAGTCTGTGCGGACCGGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC	290
Qy	298	CTGTCGCGGATCTGGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	357
Db	291	CTGTCGCGGATCTGGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	350
Qy	358	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	417
Db	351	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	410
Qy	418	AGTCTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	477
Db	411	AGTCTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	537
Db	471	CCGCCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	530

Qy	538	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC	597
Db	531	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAATTTT	1077
Db	1011	CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTATTCAATTTT	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370

Qy 1378 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC 1437
 |||
 Db 1371 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC 1430

Qy 1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497
 |||
 Db 1431 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1490

Qy 1498 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1557
 |||
 Db 1491 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1550

Qy 1558 TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT 1617
 |||
 Db 1551 TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT 1610

Qy 1618 TAAACAAAATGAAACATTTGCCAAAAACAAAACAAAAACTATGTATTTGCACAGCACAC 1677
 |||
 Db 1611 TAAACAAAATGAAACATTTGCCAAAAACAAAACAAAAACTATGTATTTGCACAGCACAC 1670

Qy 1678 TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1737
 |||
 Db 1671 TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1730

Qy 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797
 |||
 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790

Qy 1798 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1857
 |||
 Db 1791 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1850

Qy 1858 ACTTAGGCTTAAAAATGAGCTCA 1880
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 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

RESULT 3

US-09-016-434-1203

; Sequence 1203, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/016,434
;   FILING DATE:  HEREWITH
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Zeller, Karen J.
;   REGISTRATION NUMBER:  37,071
;   REFERENCE/DOCKET NUMBER:  PA-0002 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (650) 855-0555
;   TELEFAX:  (650) 845-4166
;   INFORMATION FOR SEQ ID NO:  1203:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1470 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   IMMEDIATE SOURCE:
;   LIBRARY:  GENBANK
;   CLONE:  g182275
US-09-016-434-1203

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Query Match          34.1%;  Score 1466.8;  DB 4;  Length 1470;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1468;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy      192  GAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 251
          |||
Db      1   GAAACTGCGGACGGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 60

Qy      252  AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTG 311
          |||
Db      61  AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTG 120

Qy      312  GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 371
          |||
Db      121  GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 180

Qy      372  AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 431
          |||
Db      181  AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 240

Qy      432  GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 491
          |||
Db      241  GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 300

Qy      492  CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 551
          |||
Db      301  CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 360

Qy      552  GGTGTGTCTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT 611

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Db	361	 GGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAAT	420
Qy	612	TATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT	671
Db	421	 TATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT	480
Qy	672	GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA	731
Db	481	 GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA	540
Qy	732	GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGT	791
Db	541	 GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGT	600
Qy	792	GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC	851
Db	601	 GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC	660
Qy	852	TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT	911
Db	661	 TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT	720
Qy	912	TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	971
Db	721	 TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	780
Qy	972	GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	1031
Db	781	 GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	840
Qy	1032	CATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTAGTTTTCTATTTCTGCTTGCC	1091
Db	841	 CATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTAGTTTTCTATTTCTGCTTGCC	900
Qy	1092	ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG	1151
Db	901	 ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG	960
Qy	1152	TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT	1211
Db	961	 TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT	1020
Qy	1212	CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT	1271
Db	1021	 CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT	1080
Qy	1272	GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT	1331
Db	1081	 GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT	1140
Qy	1332	GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAAACCAATTGC	1391
Db	1141	 GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAAACCAATTGC	1200
Qy	1392	TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG	1451


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Db      1201 TCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTATGCTGCTGGTG 1260
Qy      1452 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1511
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1320
Qy      1512 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1571
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1380
Qy      1572 GAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAACAAAATGAA 1631
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAACAAAATGAA 1440
Qy      1632 ACATTTGCCAAAACAAAACAAAAAACTATG 1661
        |||||||||||||||||||||||||||||||
Db      1441 ACATTTGCCAAAACAAAACAAAAAACTATG 1470

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RESULT 4

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US-09-175-658B-20
; Sequence 20, Application US/09175658B
; Patent No. 6372900
; GENERAL INFORMATION:
; APPLICANT: METALLINOS, DANIKA
; APPLICANT: RINE, JASPER
; APPLICANT: BOWLING, ANN
; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS
; FILE REFERENCE: GOBR-110
; CURRENT APPLICATION NUMBER: US/09/175,658B
; CURRENT FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/062,562
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Horse
US-09-175-658B-20

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Query Match          24.9%; Score 1070.4; DB 4; Length 1321;
Best Local Similarity 88.7%; Pred. No. 6.1e-243;
Matches 1171; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

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Qy      227 CAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTC 286
        ||||||||||||||||||| ||| |||| |||||| |||||| ||||| |||
Db      1   CAGGTAGCAGCATGCAGCCTCTGCCAACCTGTGTGGACGCGTTCTGGTGGCGCTGATCC 60
Qy      287 TTGCCTGCGGCCTGTGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCA 346
        ||||||||| || | || || ||||| ||||| ||||||| |||||
Db      61 TTGCCTGCGGCGTGGCAGGGGTCCAGGGAGAAGAGAGGAGATTCCCGCCGGCCAGGGCCA 120
Qy      347 CTCCG---CTTTTGCAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCA 403
        ||||| ||| || | ||||||||||||||| || ||||||| |||||
Db      121 CTCCGCCACTTCTGGGGTCTGAAGAGATAATGACGCCCCCGACTAAGACCTCCTGGCCGA 180

```

Qy	404	AGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACA	463
Db	181	CGGGGTCCAACGCCAGCGTGC CGCGGT CATCAGCACCTCCGCAAATGCCTAAAGCAGGGA	240
Qy	464	GGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGA	523
Db	241	GGACGGCGGGAGCCCAGCGACGCACCCTCCCTCCTCCCCCGTGCGAAAGAACCATCGAGA	300
Qy	524	TCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGA	583
Db	301	TCAAGGAGACTTTCAAGTACATCAACACAGTAGTGTCTTGCCTAGTGTTCGTGCTGGGCA	360
Qy	584	TCATCGGGAACTCCACACTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTC	643
Db	361	TCATCGGAAACTCCACACTGCTGAGAATCATTTACAAGAACAAAGTGCATGCGGAACGGCC	420
Qy	644	CCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCC	703
Db	421	CTAATATCTTGATCGCCAGCCTGGCTCTCCGAGACCTGCTGCAAATCATCATTGACGTCC	480
Qy	704	CTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGC	763
Db	481	CCATCAATGTCTACAAGCTGCTGGCTGAGGACTGGCCCTTTGGAGTCGAGATGTGTAAGC	540
Qy	764	TGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGA	823
Db	541	TGGTGCCTTTTCATACAGAAGGCCTCCGTGGGCATCACTGTGCTGAGTCTGTGTGCTCTAA	600
Qy	824	GTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAA	883
Db	601	GTATTGACAGATATCGAGCTGTTGCTTCTTGGAGCGAATTAAAGGAATTCGGGTTCCAA	660
Qy	884	AATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG	943
Db	661	AATGGACAGCAGTAGAAATTGTTTTAATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG	720
Qy	944	AAGCCATAGGTTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCT	1003
Db	721	AAGCCGTGGGTTTTTGATATGATTACCGCTGACTACAAAGGAAGTTATCTGCGAATCTGCC	780
Qy	1004	TGCTTCATCCCGTTTCAGAAGACAGCTTTTCATGCAGTTTACAAGACAGCAAAAGATTGGT	1063
Db	781	TGCTTCATCCCACTCAGAAAACAGCCTTCATGCAGTTTACAAGAATGCTAAGGACTGGT	840
Qy	1064	GGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAA	1123
Db	841	GGCTATTTAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACCTTGA	900
Qy	1124	TGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAA	1183
Db	901	TGACCTGTGAAATGTTGAGAAAGAAGAGTGGCATGCAAATGCTTTAAATGATCACTTAA	960
Qy	1184	AGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCT	1243
Db	961	AGCAGAGAAGGGAAGTGGCGAAAACAGTATTCTGCCTGGTCCTTGTCTTTGCCCTGTGCT	1020
Qy	1244	GGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCA	1303

Db	1021	GGCTTCCTCTTCACCTCAGCAGGATTTTGAAACACACTCTTTATGATCAGAATGATCCCC	1080
Qy	1304	ATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTT	1363
Db	1081	ATAGATGTGAACTTTTGAGCTTTTGTGTTGGTATTGGACTACATTGGCATCAACATGGCCT	1140
Qy	1364	CACTGAATTCTGCATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC	1423
Db	1141	CCCTGAATTCTGCATTAATCCAATAGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC	1200
Qy	1424	GCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGG	1483
Db	1201	GCTTTAAGTCGTGCTTATGCTGCTGGTGCCAATCATTTGAAGAAAAACAGTCCTTGGAAG	1260
Qy	1484	AAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA	1543
Db	1261	ACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA	1320

US-09-016-434-1257

; Sequence 1257, Application US/09016434

; Patent No. 6500938

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; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
```

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

10 TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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; MEDIUM TYPE:  floppy disk
; COMPUTER:  IBM PC compatible

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;      COMPUTER:      IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

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; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

```

; INFORMATION FOR SEQ ID NO: 1257:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4079 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g219649
US-09-016-434-1257

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Query Match          9.2%; Score 395.8; DB 4; Length 4079;
Best Local Similarity 65.7%; Pred. No. 1.3e-83;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564
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Db      685 TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 744

Qy      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      745 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 804

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      805 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 864

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      865 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 924

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      925 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTCGAGAAGTCCTCG 984

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      985 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC 1044

Qy      850 TCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1045 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAAGTACCATTGAAATTGTCTCC 1104

Qy      910 ATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTTGATATAATTACG 969
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1105 ATCTGGATCCTGTCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTTCATGGTACCC 1164

Qy      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT 1029
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1165 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1218

Qy      1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCACTTTCTATTTCTGCTTG 1089
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      1219 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCATTTCTGTATG 1278

Qy      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146
      || | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Db	1279	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1338
Qy	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Db	1339	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1398
Qy	1207	ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG	1266
Db	1399	ACAGTTTTCTGCTTGGTTGTAATTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT	1458
Qy	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT	1326
Db	1459	ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1518
Qy	1327	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1386
Db	1519	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1578
Qy	1387	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC	1446
Db	1579	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1638
Qy	1447	TGGTG	1451
Db	1639	TGCTG	1643

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RESULT 6
US-08-121-446-1
; Sequence 1, Application US/08121446
; Patent No. 6313276
; GENERAL INFORMATION:
; APPLICANT: IMURA, HIROO
; APPLICANT: NAKAO, KAZUWA
; APPLICANT: NAKANISHI, SHIGETADA
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:

```

```

;      NAME:  CIOTTI, THOMAS E.
;      REGISTRATION NUMBER:  21,013
;      REFERENCE/DOCKET NUMBER:  29900-20324.00
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  4105 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  485..1768
;      FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  545
US-08-121-446-1

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Query Match          9.2%;  Score 395.8;  DB 4;  Length 4105;
Best Local Similarity 65.7%;  Pred. No. 1.3e-83;
Matches 634;  Conservative 0;  Mismatches 307;  Indels 24;  Gaps 3;

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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564
        |||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      689 TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAAC 624
        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC 808

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
        ||  ||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG 988

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
        |||||  |||||  ||  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
        ||  |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1049 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCCTTTGGTAACTGCCATTGAAATTGTCTCC 1108

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
        ||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1109 ATCTGGATCCTGTCCTTTATCCTGGCCATTCCCTGAAGCGATTGGCTTCGTATGGTACCC 1168

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Qy 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029
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 Db 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222

Qy 1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG 1089
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282

Qy 1090 CCATTGGCCATCACTGCATTTTTTTTATACTAATGACCTGTGAAATGTTG---AGAAAG 1146
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342

Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402

Qy 1207 ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG 1266
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1403 ACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462

Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT 1326
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1463 ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522

Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1523 TTAAGTCTCATGGATTACATCGGTATTAAGTGGCAACCATGAATTCATGTATAAACCCC 1582

Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642

Qy 1447 TGGTG 1451
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 Db 1643 TGCTG 1647

RESULT 7

PCT-US92-02091-1

; Sequence 1, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/02091
;   FILING DATE:  19920313
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/426,150
;   FILING DATE:  24-OCT-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/533,659
;   FILING DATE:  05-JUN-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Ching, Edwin P.
;   REGISTRATION NUMBER:  34090
;   REFERENCE/DOCKET NUMBER:  A-0092C
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-266-7476
;   TELEFAX:  415-266-7400
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1700 base pairs
;   TYPE:  NUCLEIC ACID
;   STRANDEDNESS:  double
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   HYPOTHETICAL:  NO
;   ORIGINAL SOURCE:
;   ORGANISM:  Mus musculus
;   CELL LINE:  Swiss 3T3
;   IMMEDIATE SOURCE:
;   LIBRARY:  Lambda GT10
;   FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  378..1532
PCT-US92-02091-1

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Query Match          3.1%;  Score 132.2;  DB 5;  Length 1700;
Best Local Similarity 56.9%;  Pred. No. 1.4e-21;
Matches 242;  Conservative 0;  Mismatches 183;  Indels 0;  Gaps 0;

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Qy      535 TTCAAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAC 594
        ||||  ||  |||  |  |  |||  |  ||||  |  ||  |  ||  |||
Db      495 TTCATCTATGTCATCCCTGCAGTTTATGGGCTTATCATCGTGATAGGTCTTATTGGCAAC 554

Qy      595 TCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTG 654
        |||  ||  |  |  ||  |||  ||  |  ||||  |||||  ||||  ||  ||  ||
Db      555 ATCACGCTCATCAAGATCTTCTGCACGGTCAAGTCCATGCGAAACGTGCCAAACCTGTTC 614

Qy      655 ATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTC 714
        |||  |  |||  ||||  |||||  |||||  |||||  |||  |  ||||  |||  |
Db      615 ATCTCTAGCCTGGCTTTGGGAGACCTGCTGCTGCTGGTGACATGCGCCCCCTGTGGATGCC 674

Qy      715 TACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTC 774
        ||||  ||||  ||  ||||  |||||  |||||  ||  ||  |||  |  ||  ||
Db      675 AGCAAGTACCTGGCTGACAGGTGGCTATTTGGCAGAATTGGCTGCAAACCTGATCCCCTTT 734

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Qy 775 ATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGA 834
 ||||| | || ||||| | |||| | | || ||||| |||||
 Db 735 ATACAACTTACTTCAGTGGGGGTGTCTGTCTTCACACTTACGGCACTGTCTGAGCTGACAGG 794
 Qy 835 TATCGAGCTGTTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCA 894
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 Db 795 TACAAAGCCATTGTACGGCCAATGGATATCCAGGCATCCCATGCCCTGATGAAGATCTGT 854
 Qy 895 GTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGT 954
 | || | ||||| ||| | ||||| || | |||| | ||| | |||
 Db 855 CTCAAAGCTGCTTTGATCTGGATTGTCTCTATGTTGTTGGCCATCCAGAGGCTGTGTTT 914
 Qy 955 TTTGA 959
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 Db 915 TCTGA 919

RESULT 8

US-08-724-394A-20

; Sequence 20, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Kronmal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

; TITLE OF INVENTION: Sequences and Antibodies Thereto

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,394A

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitts, Renee A.

; REGISTRATION NUMBER: 35,136

; REFERENCE/DOCKET NUMBER: 017957-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

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;   LENGTH: 246240 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: 1..246240
;     OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

```

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 1.8e-16;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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Qy      5 CATTCCGGTGGGGGACTCTGGCCAGCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
      ||| || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db    180691 CATCCCTACGGGGAAGTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy     65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db    180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy    125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db    180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

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RESULT 9

US-08-724-394A-21

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; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
;   APPLICANT: Feder, John N.
;   APPLICANT: Kronmal, Gregory S.
;   APPLICANT: Lauer, Peter M.
;   APPLICANT: Ruddy, David A.
;   APPLICANT: Thomas, Winston
;   APPLICANT: Tsuchihashi, Zenta
;   APPLICANT: Wolff, Roger K.
;   TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
;   TITLE OF INVENTION: Sequences and Antibodies Thereto
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
;     STREET: Two Embarcadero Center, 8th Floor
;     CITY: San Francisco
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 1.8e-16;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
   ||| || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db    180691 CATCCCTACGGGGAACCTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db    180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db    180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

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RESULT 10

US-08-724-394A-22

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; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto

```

```

; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 1.8e-16;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

```

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Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
  ||| ||  |||| ||||  ||||  ||||  ||  |||  |||||  ||||| |||
Db 180691 CATCCCTACGGGAACTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
  ||||  ||||| ||||| |||||  ||||| |||  ||||| |||||  ||||| |||
Db 180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
  ||||  ||||| ||||| |||||  ||||| |||||  ||||  |||  |
Db 180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

```

RESULT 11

PCT-US92-02091-5
; Sequence 5, Application PC/TUS9202091
; GENERAL INFORMATION:
; APPLICANT: Battey Jr., James F.
; APPLICANT: Corjay, Martha H.
; APPLICANT: Feldman, Richard I.
; APPLICANT: Harkins, Richard N.
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edwin P. Ching
; STREET: 1501 Harbor Bay Parkway
; CITY: Alameda
; STATE: CA
; COUNTRY: USA
; ZIP: 94501
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02091
; FILING DATE: 19920313
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/426,150
; FILING DATE: 24-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/533,659
; FILING DATE: 05-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34090
; REFERENCE/DOCKET NUMBER: A-0092C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-266-7476
; TELEFAX: 415-266-7400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; TISSUE TYPE: Esophagus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 132..1304
PCT-US92-02091-5

Query Match 2.5%; Score 108.8; DB 5; Length 1584;
Best Local Similarity 54.8%; Pred. No. 4.3e-16;
Matches 215; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy	572	TCGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAACAAGTGCA	631
Db	292	TCTCGGTGGGCTTGCTGGGCAACATCATGCTGGTGAAGATATTCTCACCACAGCACCA	351
Qy	632	TGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCG	691
Db	352	TGCGGAGTGTCCCCAACATCTTCATCTCTAACCTGGCTGCGGGAGACCTGCTGCTGCTGC	411
Qy	692	TCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTG	751
Db	412	TGACCTGCGTCCCAGTGGATGCCTCCCGATACTTCTTTGATGAATGGGTGTTCCGCAAGC	471
Qy	752	AGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTC	811
Db	472	TGGGCTGCAAACATCCCAGCCATCCAGCTCACCTCGGTGGGGGTTTCCGTGTTCACTC	531
Qy	812	TATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGAGTAGAATTAAAGGAA	871
Db	532	TCACGGCCCTCAGCGCTGACAGGTACAGAGCTATCGTGAACCCCATGGACATGCAGACGT	591
Qy	872	TTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTC	931
Db	592	CTGGTGTGGTGTGTGGACCAGTTTGAAGGCCGTGGGCATCTGGGTGGTCTCTGTGCTGT	651
Qy	932	TGGCTGTCCCTGAAGCCATAGGTTTTGATATA	963
Db	652	TGGCTGTCCCTGAGGCTGTGTTTTTCGGAAGTA	683

RESULT 12

US-09-175-658B-25/c

; Sequence 25, Application US/09175658B

; Patent No. 6372900

; GENERAL INFORMATION:

; APPLICANT: METALLINOS, DANIKA

; APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

; CURRENT APPLICATION NUMBER: US/09/175,658B

; CURRENT FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 60/062,562

; PRIOR FILING DATE: 1997-10-21

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 801

; TYPE: DNA

; ORGANISM: Horse

; FEATURE:

; OTHER INFORMATION: Uncertain of the nucleotide sequence at positions

; OTHER INFORMATION: 30, 54, 286, 436, 445, 542, 614, 617, 624, 641,

; OTHER INFORMATION: 731, 746, 753, 770, 775 and 793.

US-09-175-658B-25

Query Match

2.5%; Score 107.2; DB 4; Length 801;

Best Local Similarity 86.8%; Pred. No. 7.6e-16;
Matches 118; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      1408 AAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAA 1467
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Db      223 AAACGAGTTATTTGTTTTGTACAGTCGTGCTTATGCTGCTGGTGCCAATCATTTGAAGAA 164

Qy      1468 AAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATAT 1527
        ||| ||| ||| || | | | | | | | | | | | | | | | | | | | | | |
Db      163 AAACAGTCCTTGAAGACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATAT 104

Qy      1528 GACAACTTCCGTTCCA 1543
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Db      103 GACAACTTCCGTTCCA 88
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RESULT 13

US-09-120-772-1

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; Sequence 1, Application US/09120772
; Patent No. 6143521
; GENERAL INFORMATION:
;   APPLICANT: LANE, PAMELA
;   APPLICANT: TSUI, PING
;   APPLICANT: ELSHOUBAGY, NABIL
;   TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE
;   TITLE OF INVENTION: 3
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Ratner & Prestia
;     STREET: P.O. Box 980
;     CITY: Valley Forge
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19482
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/120,772
;     FILING DATE: 22-JUL-1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Prestia, Paul F
;     REGISTRATION NUMBER: 23,031
;     REFERENCE/DOCKET NUMBER: GP-70505
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 610-407-0700
;     TELEFAX: 610-407-0700
;     TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1205 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-120-772-1

Query Match 2.5%; Score 106.6; DB 3; Length 1205;
Best Local Similarity 48.5%; Pred. No. 1.3e-15;
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

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Qy      578 TGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAACAGTGCATGCGAA 637
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Db      181 TGGGCATCCTTGGAAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 240

Qy      638 ACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTG 697
      | ||| ||||| ||| ||| ||||| ||||| ||||| ||| | | | | |
Db      241 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 300

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
      | || | | ||| | | ||||| | ||||| ||||| | | | | |
Db      301 GTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTCCGAAGAATTGGTT 360

Qy      758 GTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTG 817
      ||||| || | ||||| || | | | | | | | | | | | | | |
Db      361 GTAAGGTGCTCTCTTTTCATCCGGCTCACTTCTGTTGGTGTGTGAGTGTTCATTAGCAA 420

Qy      818 CTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGG 877
      ||| || ||||| || ||||| | | | | | | | | | | |
Db      421 TTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAGCCCTCCAATG 480

Qy      878 TTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTG 937
      ||| || ||||| || || || ||||| || ||||| || |||||
Db      481 CCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTGTCTATGATATTTGCTC 540

Qy      938 TCCCTGAAGCCATAGGTTTTGATATA-----ATTACGATGGACTACAAAGGAAGTTATCT 992
      | ||||| || ||| || || || || || || || || || || || |
Db      541 TACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCCAATAAAAATATGACAT 600

Qy      993 GCGAATCTGCTTGCT-TCATCCCGTTTCAAGACAGCTTTTCATGCAGTTTACAAGACAG 1051
      ||||| | || || ||||| || ||||| || || || || || |
Db      601 TTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAAGAAATACATTCTCTGC 660

Qy      1052 CAAAAGATTGGTGGCTGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTT 1111
      | | | | | | | | ||| | | | | | | | | | | |
Db      661 TGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCTGTCTACTATTCCTTGA 720

Qy      1112 TTTATACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAA 1171
      || || | | | | | ||| | | ||| || || | | | |
Db      721 TTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCC 780

Qy      1172 ATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCT 1231
      | | || | | | || | || ||||| || ||||| || || || |
Db      781 GTAAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTGGTGTGGTGGCTCTGT 840

Qy      1232 TTGCCCTCTGCTGGCTTCCCTTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATC 1291
      ||||| ||||| || || ||||| || || || || || || || |
Db      841 TTGCCCTCTGCTGGTTGCCAAATCACCTC-----CTGTACCTCTACCATTCAATTCA 891
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Qy 1292 AGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTA 1351
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 Db 892 CTTCTCAAACCTATGTA--GACCCCTCTGCCATGCATTTTCATTTTCACCATTTTCTCTC 948
 Qy 1352 TCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGCAAAA 1411
 | | | | | | | | | | | | | | | | | | | |
 Db 949 GGGTTTTGGCTTTTCAGCAATTCTTGCCTAAACCCCTTTGCTCTCTACTGGCTGAGCAAAA 1008
 Qy 1412 GATTCAAAAAGCTTTTAAGTCATGCTTATGCTGCTG 1448
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 Db 1009 GCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTG 1045

RESULT 14

US-09-016-434-1275

; Sequence 1275, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HERewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1275:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1413 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g291876
US-09-016-434-1275

Query Match 2.5%; Score 106.6; DB 4; Length 1413;
Best Local Similarity 48.5%; Pred. No. 1.4e-15;
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

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Qy      578 TGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAACAGTGCATGCGAA 637
      ||||| ||| | ||| | | | | | | | | | | | | | | | | | |
Db      328 TGGGCATCCTTGGAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAA 387

Qy      638 ACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTG 697
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      388 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 447

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
      | | | | | | | | | | | | | | | | | | | | | |
Db      448 GTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTTGGGAAGAATTGGTT 507

Qy      758 GTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTG 817
      ||||| || | | ||||| | | | | | | | | | | | | |
Db      508 GTAAGGTGCTCTCTTTTCATCCGGCTCACTTCTGTTGGTGTGTGAGTGTTACATTAAACAA 567

Qy      818 CTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGG 877
      ||| | | | ||||| | | | | | | | | | | | | |
Db      568 TTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAGCCCTCCAATG 627

Qy      878 TTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTG 937
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Db      628 CCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTGTCTATGATATTTGCTC 687

Qy      938 TCCCTGAAGCCATAGGTTTTGATATA-----ATTACGATGGACTACAAAGGAAGTTATCT 992
      | | |||| | | | | | | | | | | | | | | | | |
Db      688 TACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCCAATAAAAATATGACAT 747

Qy      993 GCGAATCTGCTTGCT-TCATCCCGTTTCAAGACAGCTTTTCATGCAGTTTACAAGACAG 1051
      ||||| | | | | | | | | | | | | | | | | |
Db      748 TTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAAGAAATACATTCTCTGC 807

Qy      1052 CAAAAGATTGGTGGCTGTTTCACTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTT 1111
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Db      808 TGTGCTTCTTAGTGTTCTACATTATTCCACTCTCTATTATCTCTGTCTACTATTCTTGA 867

Qy      1112 TTTATACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAA 1171
      || | | | | | | | | | | | | | | | | |
Db      868 TTGCTAGGACCTTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCC 927

Qy      1172 ATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCT 1231
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Db      928 GTAAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTGGTGTGGTGGCTCTGT 987

Qy      1232 TTGCCCTCTGCTGGCTTCCCTTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATC 1291
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Db      988 TTGCCCTCTGCTGGTTGCCAAATCACCTC-----CTGTACCTCTACCATTATTCA 1038
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Qy 1292 AGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTA 1351
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 Db 1039 CTTCTCAAACCTATGTA---GACCCCTCTGCCATGCATTTTCATTTTCACCATTTTCTCTC 1095
 Qy 1352 TCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGCAAAA 1411
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 Db 1096 GGGTTTGGCTTTTCAGCAATTCTTGCCTAAACCCCTTTGCTCTCTACTGGCTGAGCAAAA 1155
 Qy 1412 GATTCAAAAAGCTTTTAAGTCATGCTTATGCTGCTG 1448
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 Db 1156 GCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTG 1192

RESULT 15

US-09-016-434-1215

; Sequence 1215, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HERewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1215:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1726 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:

; LIBRARY: GENBANK
; CLONE: g183649
US-09-016-434-1215

Query Match 2.5%; Score 106; DB 4; Length 1726;
Best Local Similarity 52.0%; Pred. No. 2.1e-15;
Matches 238; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

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Db      514 TCCTCTATGTCATCCCTGCAGTTTATGGGGTTATCATTCTGATAGGCCTCATTGGCAACA 573

Qy      596 CCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGA 655
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Db      574 TCACTTTGATCAAGATCTTCTGTACAGTCAAGTCCATGCGAAACGTTCCAAACCTGTTCA 633

Qy      656 TCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCT 715
      | |||| | |||| | |||| | |||| | || || || || || || || || || || ||
Db      634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCCTCCTAATAACGTGTGCTCCAGTGCGATGCCA 693

Qy      716 ACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCA 775
      || | |||| | | || || |||| | || || || || || || || || || || ||
Db      694 GCAGGTACCTGGCTGACAGATGGCTATTTGGCAGGATTGGCTGCAAACCTGATCCCCTTTA 753

Qy      776 TACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGAT 835
      |||| | |||| | || | |||| | | || || || || || || || || || || ||
Db      754 TACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACTCACGGCGCTCTCGGCAGACAGAT 813

Qy      836 ATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAG 895
      | || | || | | | | || || || || || || || || || || || || || ||
Db      814 ACAAAGCCATTGTCCGGCCAATGGATATCCAGGCCTCCCATGCCCTGATGAAGATCTGCC 873

Qy      896 TAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTT 955
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Db      874 TCAAAGCCGCCTTTATCTGGATCATCTCCATGCTGCTGGCCATTCCAGAGGCCGTGTTTT 933

Qy      956 TTGATATAATTACGATGGACTACAAAGGAAGTTATCTG 993
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Search completed: December 13, 2003, 00:00:18
Job time : 264.387 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 10:54:32 ; Search time 1259.7 Seconds
(without alignments)
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Title: US-09-931-157-2
Perfect score: 4301
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

	1	4301	100.0	4301	9	US-09-931-157-2	Sequence 2, Appli
	2	4284.4	99.6	4286	13	US-10-007-926A-177	Sequence 177, App
	3	4284.4	99.6	4286	13	US-09-921-406C-13	Sequence 13, Appl
	4	4284.4	99.6	4286	13	US-10-210-120-15	Sequence 15, Appl
	5	4284.4	99.6	4286	15	US-10-225-567A-113	Sequence 113, App
c	6	2841.8	66.1	183337	15	US-10-020-141-5	Sequence 5, Appli
	7	1322.6	30.8	1329	13	US-09-826-509-496	Sequence 496, App
	8	763.2	17.7	800	9	US-09-778-927A-27	Sequence 27, Appl
c	9	440.6	10.2	592	9	US-09-962-436-531	Sequence 531, App
c	10	440.6	10.2	592	10	US-09-880-107-2060	Sequence 2060, Ap
c	11	440.6	10.2	592	10	US-09-954-531-917	Sequence 917, App
	12	403.4	9.4	405	11	US-09-918-995-7311	Sequence 7311, Ap
	13	395.8	9.2	4105	9	US-09-931-157-1	Sequence 1, Appli
	14	395.8	9.2	4105	13	US-10-007-926A-229	Sequence 229, App
	15	395.8	9.2	4105	13	US-10-101-510-370	Sequence 370, App
	16	395.8	9.2	4105	15	US-10-225-567A-115	Sequence 115, App
	17	392.6	9.1	1284	13	US-09-826-509-494	Sequence 494, App
	18	311	7.2	390	13	US-10-007-926A-176	Sequence 176, App
c	19	302	7.0	363	9	US-09-962-436-533	Sequence 533, App
c	20	302	7.0	363	10	US-09-954-456-209	Sequence 209, App
c	21	302	7.0	363	10	US-09-954-456-467	Sequence 467, App
c	22	302	7.0	363	10	US-09-954-456-925	Sequence 925, App
c	23	302	7.0	363	10	US-09-954-456-1550	Sequence 1550, Ap
c	24	302	7.0	363	10	US-09-880-107-2076	Sequence 2076, Ap
c	25	302	7.0	363	13	US-09-873-367C-129	Sequence 129, App
c	26	275	6.4	307	13	US-09-921-406C-12	Sequence 12, Appl
	27	148.8	3.5	1889	10	US-09-867-701-10875	Sequence 10875, A
	28	131.6	3.1	1330	11	US-09-374-046A-151	Sequence 151, App
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	30	128.4	3.0	858	15	US-10-198-846-12892	Sequence 12892, A
	31	128.4	3.0	888	13	US-10-264-283-93	Sequence 93, Appl
	32	128.2	3.0	668	15	US-10-198-846-13575	Sequence 13575, A
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	34	127.8	3.0	1926	13	US-09-814-353-21277	Sequence 21277, A
c	35	124.8	2.9	1096	13	US-09-814-353-21728	Sequence 21728, A
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	37	122.2	2.8	1291	14	US-10-027-632-124978	Sequence 124978,
	38	118.6	2.8	489	11	US-09-918-995-136	Sequence 136, App
c	39	114.6	2.7	235033	15	US-10-301-844-1	Sequence 1, Appli
c	40	114.6	2.7	237326	15	US-10-301-844-2	Sequence 2, Appli
	41	112	2.6	2595	9	US-09-160-116-11	Sequence 11, Appl
c	42	111.6	2.6	860	15	US-10-198-846-7034	Sequence 7034, Ap
c	43	111	2.6	399	15	US-10-102-806-400	Sequence 400, App
c	44	109.8	2.6	347	13	US-09-814-353-4577	Sequence 4577, Ap
c	45	109.8	2.6	347	13	US-09-814-353-10877	Sequence 10877, A

ALIGNMENTS

RESULT 1

US-09-931-157-2

; Sequence 2, Application US/09931157

; Patent No. US20020082414A1

; GENERAL INFORMATION:

; APPLICANT: Imura, Hiroo

Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGCTGGGGATCATCGGGAACCTCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGCTGGGGATCATCGGGAACCTCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320

Qy	1321	AGCTTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAAGTATTCTACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAAGTATTCTACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATCTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATCTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACTACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTAAGTGTAATTATTTTAACTACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160

Qy	2161	TTTTGAAAAATCATTACACTTTTCACTAGAAAGCCCAAAACCTCAGCATTTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAAATCATTACACTTTTCACTAGAAAGCCCAAAACCTCAGCATTTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTGCAAAAACAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTGCAAAAACAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTAATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTTGTAATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTTCTAAGCAAAGTGCCCTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTTCTAAGCAAAGTGCCCTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060

Db	3001	 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900

Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
 Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
 Qy 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301
 ||||||||||||||||||||||||||||||||||||||||||
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301

RESULT 2

US-10-007-926A-177

; Sequence 177, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007,926A

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 60/254,090

; PRIOR FILING DATE: 2000-12-08

; NUMBER OF SEQ ID NOS: 468

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 177

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: endothelin receptor type b (EDNRB) gene.

US-10-007-926A-177

Query Match 99.6%; Score 4284.4; DB 13; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780

Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCAATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCAATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620

Qy	1621	AACAAAATGAAACATTTTGCCAAAAA CAAAA CAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTTGCCAAAAA CAAAA CAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTTAAGTGTAATTTATTTTAA CACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTTAAGTGTAATTTATTTTAA CACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTG GGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTG GGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTTACAGTTAGCACTTCAACATAG CTCTTAA CAACTTCCAGGATATTACACAACACT	1860
Db	1801	TTTTTTACAGTTAGCACTTCAACATAG CTCTTAA CAACTTCCAGGATATTACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAAT TTTCTATTCTTTCTAAAAAGAGATTTATTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAAT TTTCTATTCTTTCTAAAAAGAGATTTATTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATATAAAGGA AGAATAAGTCACTGTAAAA CAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATATAAAGGA AGAATAAGTCACTGTAAAA CAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAAT TTTAAAAATCCTTTAAAA CAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAAT TTTAAAAATCCTTTAAAA CAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAG ATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAG ATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATG ATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATG ATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAG AAGCCCAAACCTCAGCATTTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAG AAGCCCAAACCTCAGCATTTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAA CAGACTGGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAA CAGACTGGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTAC ATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTAC ATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCT ATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCT ATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACA ATTTTTTCAGGATTATTAAATCTTCTTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACA ATTTTTTCAGGATTATTAAATCTTCTTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGT TTTGTGCATCTGTAAATACTTACCTACATACA	2520

Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360

Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACTTGTTCTTTAATTTATCCCAATCACTTTTTAGAGGCCTGTTATCATAGAAGT 3420
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Db 3361 ACAAACTTGTTCTTTAATTTATCCCAATCACTTTTTAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTACAGTTTATTAA 3480
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Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTACAGTTTATTAA 3480

Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540
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Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540

Qy 3541 TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600
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Db 3541 TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660
 |||

Db 3601 TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660

Qy 3661 TTTAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720
 |||

Db 3661 TTTAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780
 |||

Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAATCATGGATGTTA 3840
 |||

Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAATCATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900
 |||

Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
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Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
 |||

Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
 |||

Db 4021 AAAAAATTATATATCTGGGAGGATTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140
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Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200
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Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200

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Qy      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
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Db      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

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RESULT 3

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US-09-921-406C-13
; Sequence 13, Application US/09921406C
; Publication No. US20030152923A1
; GENERAL INFORMATION:
; APPLICANT: Yakhini, Zohar
; APPLICANT: Ben-Dor, Amir
; APPLICANT: Sampas, Nick
; APPLICANT: Dougherty, Edward
; APPLICANT: Trent, Jeff
; APPLICANT: Meltzer, Paul
; APPLICANT: Chen, Yidong
; APPLICANT: Weeraratna, Ashani
; APPLICANT: Jiang, Yuan
; APPLICANT: Bittner, Michael
; TITLE OF INVENTION: Classifying Cancers
; FILE REFERENCE: 10010313-1
; CURRENT APPLICATION NUMBER: US/09/921,406C
; CURRENT FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-921-406C-13

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Query Match          99.6%; Score 4284.4; DB 13; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

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Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140

Db	1081	 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAAACAGAACCTTTTAAATG	1980

Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820

Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAACCTGCTTTTGTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAACCTGCTTTTGTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCTGTATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCTGTATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT	3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720
 |||
 Db 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780
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 Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840
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 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
 |||
 Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
 |||
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
 |||
 Db 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
 |||
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140
 |||
 Db 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
 |||
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
 |||
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
 |||
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 4

US-10-210-120-15

; Sequence 15, Application US/10210120

; Publication No. US20030175736A1

; GENERAL INFORMATION:

; APPLICANT: Chinnaiyan, Arul M.

; APPLICANT: Rubin, Mark A.

; APPLICANT: Sreekumar, Arun

; TITLE OF INVENTION: Expression Profile of Prostate Cancer

; FILE REFERENCE: UM-07221

; CURRENT APPLICATION NUMBER: US/10/210,120

; CURRENT FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-15

Query Match 99.6%; Score 4284.4; DB 13; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAC TGGTACTTGGAGTCTGGACATCTGA 180
      |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAC TGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
      |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
      |||
Db    481 CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy    541 TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAC TCCACA 600
      |||
Db    541 TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAC TCCACA 600

Qy    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
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Db	601	 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTC	1260
Db	1201	 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	1381	 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAAGCAGTCGTGCTTA	1500

Db	1441	TGCTGCTGGTGCCAGTCAATTTGAAGAAAAACAGTCCCTTGGAGGAAAAAGCAGTCGTCGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACCTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACCTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTCAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTCAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTAAGTCAATTTTAAATTTTAAATCCTTTTAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTAAGTCAATTTTAAATTTTAAATCCTTTTAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTTCGGACACTGGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAAGACAAAGGCTGT	2160
Db	2101	TTTTTCGGACACTGGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAAGACAAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340

Qy	2341	CAAAAGAGAAAATAGAATGTTTGGAAAGGCTATCCCAAAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAAGAGAAAATAGAATGTTTGGAAAGGCTATCCCAAAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACCTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACCTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA	3180

Qy	3181	ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAGATTATATAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAGATTATATAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080

Db	4021		AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081		TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC	4140
Db	4081		TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC	4140
Qy	4141		ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141		ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201		CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201		CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261		AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261		AAAATGCCACATTTCTGGTCTCTGGG	4286

RESULT 5

US-10-225-567A-113

; Sequence 113, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 113

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-225-567A-113

Query Match 99.6%; Score 4284.4; DB 15; Length 4286;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1		60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61		120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA	180

Db	121	 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA	540
Db	481	CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG	1020

Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACCTGAATTCCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACCTGAATTCCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCCTGGAGGAAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCCTGGAGGAAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTCACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAAACAACTTCCAGGATATTACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAAACAACTTCCAGGATATTACACAACACT	1860

Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700

Qy	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAAATTTTTATATCTTCTAAGCAAAGTGCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAAATTTTTATATCTTCTAAGCAAAGTGCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Qy	3181	ATTTTACTTTGTTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTACTTTGTTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAAGAGCAATAATAATTAAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAAGAGCAATAATAATTAAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTTCTCCATGTGAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600

Db	3541	 TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	 TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	 TTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	 TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	 AAAATGCCACATTTCTGGTCTCTGGG	4286

RESULT 6

US-10-020-141-5/c

; Sequence 5, Application US/10020141

; Publication No. US20030092013A1

; GENERAL INFORMATION:

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; APPLICANT: McCarthy, Jeanette
; APPLICANT: Ableson, Allen
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-002
; CURRENT APPLICATION NUMBER: US/10/020,141
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/313,097
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/327,485
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 183337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-020-141-5

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Query Match          66.1%; Score 2841.8; DB 15; Length 183337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2854; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72830 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 72771

Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72770 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 72711

Qy      1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC 1609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72710 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC 72651

Qy      1610 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAAACAAAAACAAAAACTATGTATTTGCA 1669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72650 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAAACAAAAACAAAAACTATGTATTTGCA 72591

Qy      1670 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTACTCACAGCTACATATGACATT 1729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72590 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTACTCACAGCTACATATGACATT 72531

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 1789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72530 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 72471

Qy      1790 AAGCACTTAATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72470 AAGCACTTAATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 72411

Qy      1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAG 1909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72410 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAG 72351

Qy      1910 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGA 1969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72350 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGA 72291

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Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTTAAAAACAACCTTT	2029
Db	72290	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTTAAAAACAACCTTT	72231
Qy	2030	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	2089
Db	72230	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	72171
Qy	2090	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG	2149
Db	72170	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG	72111
Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	2209
Db	72110	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	72051
Qy	2210	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	72050	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	71991
Qy	2270	TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTTACATTTCAGTTAAG	2329
Db	71990	TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTTACATTTCAGTTAAG	71931
Qy	2330	ATCAAACCTCACAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAA	2389
Db	71930	ATCAAACCTCACAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAA	71871
Qy	2390	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA	2449
Db	71870	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA	71811
Qy	2450	ATCTTCTTTTTTTCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	71810	ATCTTCTTCTTTTCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	71751
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTTAC	2569
Db	71750	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTTAC	71691
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCAC	2629
Db	71690	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCAC	71631
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	2689
Db	71630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	71571
Qy	2690	ATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	2749
Db	71570	ATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	71511
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	71510	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	71451

Qy	2810	AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAACCTGCTTTTTTGAGACCGT	2869
Db	71450	AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAACCTGCTTTTTTGAGACCGT	71391
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCT	2929
Db	71390	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCT	71331
Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	2989
Db	71330	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	71271
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	3049
Db	71270	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	71211
Qy	3050	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTG	3109
Db	71210	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTG	71151
Qy	3110	CAATGTTCTCAGAGTGACTTTTGGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	71150	CAATGTTCTCAGAGTGACTTTTGGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	71091
Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	3229
Db	71090	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	71031
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAA	3289
Db	71030	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAA	70971
Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTT	3349
Db	70970	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTT	70911
Qy	3350	ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	70910	ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	70851
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
Db	70850	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	70791
Qy	3470	CAGTTTATTAATATATTTTAAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	3529
Db	70790	CAGTTTATTAATATATTTTAAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	70731
Qy	3530	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	70730	GAATTTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	70671
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	3649
Db	70670	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	70611
Qy	3650	TTCAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	3709

Db	70610	 TTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	70552
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	70551	 ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	70492
Qy	3770	TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	3829
Db	70491	 TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	70432
Qy	3830	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	3889
Db	70431	 CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	70372
Qy	3890	CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	70371	 CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	70312
Qy	3950	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	70311	 AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	70252
Qy	4010	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069
Db	70251	 TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	70192
Qy	4070	GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACAATA	4129
Db	70191	 GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACAATA	70132
Qy	4130	CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA	4189
Db	70131	 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA	70072
Qy	4190	TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	4249
Db	70071	 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	70012
Qy	4250	GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	4286
Db	70011	 GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	69975

RESULT 7

US-09-826-509-496

; Sequence 496, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	601	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	660
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	661	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	720
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	721	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	780
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	781	CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	840
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	841	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	900
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	901	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	960
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCAC	1257
Db	961	GTGAAGAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCAC	1020
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1021	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1080
Qy	1318	TTGAGCTTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1081	TTGAGCTTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1140
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1437
Db	1141	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1200
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC	1497
Db	1201	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC	1260
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1557
Db	1261	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1320
Qy	1558	TCATCTTGA	1566
Db	1321	TCATCTTGA	1329

RESULT 8

; Sequence 27, Application US/09778927A

; Patent No. US20020068342A1


```

; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(800 )
; OTHER INFORMATION: n = a,c,g,t any unknown or other
US-09-778-927A-27

```

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Query Match          17.7%; Score 763.2; DB 9; Length 800;
Best Local Similarity 98.3%; Pred. No. 1.9e-144;
Matches 771; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||
Db     61 AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180
      |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
      |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||

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Db      421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
Qy      481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
Qy      541 TACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TACATCAACACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600
Qy      601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
Qy      661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
Qy      721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780
        |||||||||||||||||||||||||||||||||||||||| || || || || || ||
Db      721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGCCAGGTAGGAGCGTTACCCAC 780
Qy      781 AAAG 784
        ||
Db      781 CCAG 784

```

RESULT 9

US-09-962-436-531/c

; Sequence 531, Application US/09962436

; Patent No. US20020081301A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature Gene

; TITLE OF INVENTION: Sets

; FILE REFERENCE: 689290-75

; CURRENT APPLICATION NUMBER: US/09/962,436

; CURRENT FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/60/235,082

; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/60/234,924

; PRIOR FILING DATE: 2000-09-25

; NUMBER OF SEQ ID NOS: 568

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 531

; LENGTH: 592

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: n=a,t,g or c

US-09-962-436-531

```

Query Match      10.2%;  Score 440.6;  DB 9;  Length 592;
Best Local Similarity  90.1%;  Pred. No. 3.6e-79;
Matches  525;  Conservative  0;  Mismatches  47;  Indels  11;  Gaps  5;

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; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2060
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 H97587
; NAME/KEY: unsure
; LOCATION: (1)..(592)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2060

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Query Match          10.2%; Score 440.6; DB 10; Length 592;
Best Local Similarity 90.1%; Pred. No. 3.6e-79;
Matches 525; Conservative 0; Mismatches 47; Indels 11; Gaps 5;

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```

Qy      993 GCGAATCTGCTTGCTTCATCCCGTTGAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGC 1052
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      578 GGGGAAGTGGCTGGCTCATCCNGTTGAGAAGACAGCTTNCAGCCAG--TTNCCAGGCCGG 521

Qy      1053 AAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTT 1112
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      520 CAAAAGATGGTGGCTGTCCAGTNC--AATTCCGGCTTTNCATGGCCATCACNGCA-TTTT 464

Qy      1113 TTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAA 1172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      463 TTATACACTAANGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAA 404

Qy      1173 TG---ATCACCTAAAGCAGAGACGGGAAGTGGCCAAAA---CCGTCTTTTGCCTGGTCCT 1226
      || | | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      403 TGGACCACCCTAAAGCCAGAGCCGNAAGTGGCCAAAANCCGGTCTTTTGCCTGGTCCT 344

Qy      1227 TGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 1286
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      343 GGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 284

Qy      1287 TAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATAT 1346
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      283 TAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATAT 224

Qy      1347 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 1406
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      223 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 164

Qy      1407 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 1466
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      163 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 104

Qy      1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 1526
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      103 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 44

Qy      1527 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1569
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 43 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1

RESULT 11

US-09-954-531-917/c

; Sequence 917, Application US/09954531

; Patent No. US20020165180A1

; GENERAL INFORMATION:

; APPLICANT: Weaver, Zoe

; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer

; TITLE OF INVENTION: Gene Sets

; FILE REFERENCE: 689290-77

; CURRENT APPLICATION NUMBER: US/09/954,531

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: US/60/233,133

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US/60/234,009

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,034

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,509

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US/60/234,567

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 1392

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 917

; LENGTH: 592

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(592)

; OTHER INFORMATION: n=a,t,g or c

US-09-954-531-917

Query Match 10.2%; Score 440.6; DB 10; Length 592;

Best Local Similarity 90.1%; Pred. No. 3.6e-79;

Matches 525; Conservative 0; Mismatches 47; Indels 11; Gaps 5;

```
Qy      993 GCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGC 1052
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      578 GGGGAACTGGCTGGCTCATCCNGTTCAGAAGACAGCTTNCAGCCAG--TTNCCAGGCCGG 521

Qy     1053 AAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTT 1112
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      520 CAAAAGATGGTGGCTGTCCAGTNC--AATTCGGCTTTNCATGGCCATCACNGCA-TTTT 464

Qy     1113 TTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAA 1172
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      463 TTATACACTAANGACCTGTGAAATGTTGAGAAGGAAAAGTGGCATGCAGATTGCTTTAAA 404

Qy     1173 TG---ATCACCTAAAGCAGAGACGGGGAAGTGGCCAAAA---CCGTCTTTTGCCCTGGTCCT 1226
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      403 TGGACCACCTAAAGCCAGAGCCGGNAAGTGGCCAAAAANCCGGTCTTTTGCCCTGGTCCT 344
```

Qy 1227 TGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 1286
 |||
 Db 343 GGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTA 284

Qy 1287 TAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATAT 1346
 |||
 Db 283 TAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATAT 224

Qy 1347 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 1406
 |||
 Db 223 TGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAG 164

Qy 1407 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 1466
 |||
 Db 163 CAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGA 104

Qy 1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 1526
 |||
 Db 103 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATA 44

Qy 1527 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1569
 |||
 Db 43 TGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1

RESULT 12

US-09-918-995-7311

; Sequence 7311, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 7311

; LENGTH: 405

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-918-995-7311

Query Match 9.4%; Score 403.4; DB 11; Length 405;

Best Local Similarity 99.8%; Pred. No. 9.9e-72;

Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2062 TAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATT 2121
 |||
 Db 1 TAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATT 60

Qy 2122 TAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTT 2181
 |||
 Db 61 TAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTT 120

```

Qy      2182 CACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAACCAACATGTCACAAACAAGCAG 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAACCAACATGTCACAAACAAGCAG 180

Qy      2242 CATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAATATAATACTTTTAAAAAGAAA 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAATATAATACTTTTAAAAAGAAA 240

Qy      2302 ATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCACAAAGAGAAATAGAATGTTTG 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCACAAAGAGAAATAGAATGTTTG 300

Qy      2362 AAAGGCTATCCCAAAGACTTTTTTGAATCTGTTCATTCACATACCCTGTGAAGACAATAC 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 AAAGGCTATCCCAAAGACTTTTTTGAATCTGTTCATTCACATACCCTGTGAAGACAATAC 360

Qy      2422 TATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTTTCACTA 2466
          |||||||||||||||||||||||||||||||||| ||||||||
Db      361 TATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTTCACTA 405

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RESULT 13

US-09-931-157-1

```

; Sequence 1, Application US/09931157
; Patent No. US20020082414A1
; GENERAL INFORMATION:
; APPLICANT: Imura, Hiroo
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4105
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (485)...(1768)
; NAME/KEY: sig_peptide
; LOCATION: (485)...(544)
; NAME/KEY: mat_peptide
; LOCATION: (545)...(1768)

```

US-09-931-157-1

```

Query Match          9.2%;  Score 395.8;  DB 9;  Length 4105;
Best Local Similarity 65.7%;  Pred. No. 1.3e-69;

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Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

```
Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC 564
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy      565 CTTGTGTTCTGTCTGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAAC 624
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTTTGAGAAGTCCTCG 988

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
      ||||| ||||| | | | | | | | | | | | | | | | | | | | |
Db      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1049 TCCTGGAGTCGTGTTTCAAGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATTGTCTCC 1108

Qy      910 ATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1109 ATCTGGATCCTGTCTTTATCCTGGCCATTCTCTGAAGCGATTGGCTTCGTTCATGGTACCC 1168

Qy      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT 1029
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222

Qy      1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAAGTTTCTATTTCTGCTTG 1089
      ||||| ||||| ||||| | | | | | | | | | | | | | | | | |
Db      1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCCTATTTCTGTATG 1282

Qy      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342

Qy      1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1343 AATGGCAGCTTGAGAAATGCCCCCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402

Qy      1207 ACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG 1266
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1403 ACAGTTTTCTGCTTGGTTGTAAATTTTGTCTTTTGTCTGGTTCCCTCTTCACTTAAGCCGT 1462

Qy      1267 ATTCTGAAGCTCACTCTTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTT 1326
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db      1463 ATATTGAAGAAAACTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522
```


Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386
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 Db 1523 TTACTGCTCATGGATTACATCGGTATTAAGTTGGCAACCATGAATTCATGTATAAACCCC 1582

Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642

Qy 1447 TGGTG 1451
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 Db 1643 TGCTG 1647

RESULT 14

US-10-007-926A-229

; Sequence 229, Application US/10007926A
 ; Publication No. US20030143539A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERTUCCI, FRANCOIS
 ; APPLICANT: HOULGATTE, REMI
 ; APPLICANT: BIRNBAUM, DANIEL
 ; APPLICANT: NGUYEN, CATHERINE
 ; APPLICANT: VIENS, PATRICE
 ; APPLICANT: FERT, VINCENT
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
 ; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
 ; FILE REFERENCE: 1546-R-00
 ; CURRENT APPLICATION NUMBER: US/10/007,926A
 ; CURRENT FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: 60/254,090
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 468
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 229
 ; LENGTH: 4105
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: endothelin receptor type a (EDNRA) gene.
 US-10-007-926A-229

Query Match 9.2%; Score 395.8; DB 13; Length 4105;
 Best Local Similarity 65.7%; Pred. No. 1.3e-69;
 Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

Qy 505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGC 564
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 Db 689 TGCCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy 565 CTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAAC 624
 | | | | | | | | | | | | | | | | | | | | | |
 Db 749 ACTATTTTCATCGTGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808

Qy 625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
 | | | | | | | | | | | | | | | | | | | | | |
 Db 809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGAGACCTTATC 868

Qy	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Db	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Qy	741	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	789
Db	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG	988
Qy	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Db	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC	1048
Qy	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Db	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Qy	910	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Db	1109	ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTATGGTACCC	1168
Qy	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT	1029
Db	1169	TTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA	1222
Qy	1030	TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG	1089
Db	1223	TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG	1282
Qy	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG	1146
Db	1283	CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG	1342
Qy	1147	AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA	1206
Db	1343	AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA	1402
Qy	1207	ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGG	1266
Db	1403	ACAGTTTTCTGCTTGGTTGTAATTTTGTCTTTTGCTGGTTCCTCTTCACTTAAGCCGT	1462
Qy	1267	ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGTAGCTTT	1326
Db	1463	ATATTGAAGAAAACGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC	1522
Qy	1327	CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA	1386
Db	1523	TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC	1582
Qy	1387	ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACGCTTTAAGTCATGCTTATGCTGC	1446
Db	1583	ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC	1642
Qy	1447	TGGTG 1451	
Db	1643	TGCTG 1647	

RESULT 15

US-10-101-510-370

; Sequence 370, Application US/10101510
 ; Publication No. US20030148295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WAN, JACKSON
 ; APPLICANT: WANG, YIXIN
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 ; FILE REFERENCE: 15117.0012
 ; CURRENT APPLICATION NUMBER: US/10/101,510
 ; CURRENT FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: 60/276,947
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 805
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 370
 ; LENGTH: 4105
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-101-510-370

Query Match 9.2%; Score 395.8; DB 13; Length 4105;
 Best Local Similarity 65.7%; Pred. No. 1.3e-69;
 Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

Qy	505	TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCTGC	564
Db	689	TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT	748
Qy	565	CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC	624
Db	749	ACTATTTTCATCGTGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTACCAGAAC	808
Qy	625	AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG	684
Db	809	AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC	868
Qy	685	CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC----	740
Db	869	TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT	928
Qy	741	-----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC	789
Db	929	GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG	988
Qy	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Db	989	GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCAGTTGCC	1048
Qy	850	TCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Db	1049	TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC	1108
Qy	910	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Db	1109	ATCTGGATCCTGTCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCTATGGTACCC	1168

Qy 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTGAAAGACAGCT 1029
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222

Qy 1030 TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTTG 1089
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 Db 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1282

Qy 1090 CCATTGGCCATCACTGCATTTTTTTTATACTAATGACCTGTGAAATGTTG---AGAAAG 1146
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342

Qy 1147 AAAAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402

Qy 1207 ACCGTCCTTTTGCTTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGG 1266
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1403 ACAGTTTTCTGCTTGGTTGTAATTTTTTGCTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462

Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTT 1326
 | | | | | | | | | | | | | | | | | | | | | |
 Db 1463 ATATTGAAGAAAACCTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522

Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386
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 Db 1523 TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1582

Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446
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 Db 1583 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTGTTTCCAGTCATGCCTCTGCTGC 1642

Qy 1447 TGGTG 1451
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 Db 1643 TGCTG 1647

Search completed: December 13, 2003, 00:41:45
 Job time : 1270.7 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:56 ; Search time 995.175 Seconds
(without alignments)
11666.569 Million cell updates/sec

Title: US-09-931-157-2
Perfect score: 4301
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	4297.8	99.9	4301	14	AAQ34584			ETb receptor gene.
2	4284.4	99.6	4286	21	AAF21284			Human low adenosin
3	4284.4	99.6	4286	21	AAA35162			Human adenosine re
4	4284.4	99.6	4286	24	ABV94186			Breast carcinoma r
5	4284.4	99.6	4286	25	ABZ42661			Human endothelin B
6	4284.4	99.6	13611	21	AAF21288			Human low adenosin
7	4284.4	99.6	13612	21	AAA35166			Human adenosine re
8	2857	66.4	2972	24	ABK94410			DNA encoding endot
c 9	2841.8	66.1	183337	25	ABQ77402			Human EDNRB DNA.
10	1691.8	39.3	1873	19	AAV17875			Homo sapiens endot
11	1690.8	39.3	1872	21	AAF21283			Human low adenosin
12	1690.8	39.3	1872	21	AAA35161			Human adenosine re
13	1495.4	34.8	1719	21	AAF21285			Human low adenosin
14	1495.4	34.8	1720	21	AAA35163			Human adenosine re
15	1466.8	34.1	1470	25	ACA56605			Human signalling p
16	1389	32.3	1632	24	AAD24966			Human G-protein co
17	1322.6	30.8	1329	23	ABI97988			Non-endogenous hum
18	1248	29.0	1578	25	ABX74409			Human cDNA sequenc
19	1220.4	28.4	1578	21	AAF21287			Human low adenosin
20	1220.4	28.4	1578	21	AAA35165			Human adenosine re
21	1099.2	25.6	1958	24	ABI99321			Mouse ischaemic co
22	1091	25.4	1965	13	AAQ25892			Sequence encodes e
23	1066	24.8	1406	15	AAQ53922			Bovine ET receptor
24	763.2	17.7	800	24	ABS51841			Novel human thromb
25	537.2	12.5	1752	24	ABK94409			DNA encoding endot
c 26	440.6	10.2	592	24	ABN95562			Gene #2060 used to
c 27	440.6	10.2	592	24	ABL63647			Breast cancer rela
c 28	440.6	10.2	592	24	ABL64653			Stomach cancer rel
29	395.8	9.2	1284	15	AAQ63209			Human endothelin r
30	395.8	9.2	1868	21	AAF20903			Human low adenosin
31	395.8	9.2	1868	21	AAF20915			Human endothelin r
32	395.8	9.2	1868	21	AAA34781			Human adenosine re
33	395.8	9.2	1868	21	AAA34793			Human adenosine re
34	395.8	9.2	2008	21	AAF20904			Human low adenosin
35	395.8	9.2	2008	21	AAA34782			Human adenosine re
36	395.8	9.2	4079	25	ACA56659			Human signalling p
37	395.8	9.2	4105	14	AAQ34583			ETa receptor gene.
38	395.8	9.2	4105	24	ABZ35259			Human gene express
39	395.8	9.2	4105	24	ABV94238			Breast carcinoma r
40	395.8	9.2	4105	25	ABZ42662			Human endothelin A
41	395.8	9.2	5036	21	AAF21447			Human endothelin r
42	395.8	9.2	117609	21	AAF21435			Human receptor-rel
43	395.4	9.2	4105	21	AAA38341			Human endothelin r
44	394.2	9.2	1310	21	AAF20902			Human endothelin r
45	394.2	9.2	1310	21	AAF20914			Human ELAM-1 polyn

ALIGNMENTS

RESULT 1

AAQ34584

ID AAQ34584 standard; DNA; 4301 BP.

XX

AC AAQ34584;

XX

DT 25-MAR-2003 (updated)

DT 11-MAY-1993 (first entry)

XX

DE ETb receptor gene.

XX

KW Human; ETa; ETb; endothelin; receptor; transmembrane domain; N tail;

KW extracellular; cytoplasmic; C tail; post translational; bovine;

KW modification; ET-1 receptor; antagonist; circulatory system; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	238..1566
FT		/*tag= a
FT	sig_peptide	238..315
FT		/*tag= b
FT	mat_peptide	316..1563
FT		/*tag= c
FT	polyA_signal	2595..2600
FT		/*tag= d
FT	polyA_signal	3134..3139
FT		/*tag= e
FT	polyA_signal	3638..3643
FT		/*tag= f
FT	polyA_signal	4101..4106
FT		/*tag= g
FT	polyA_signal	4258..4263
FT		/*tag= h
FT	misc_feature	1909..1913
FT		/*tag= i
FT		/function= Related with mRNA instability
FT	misc_feature	1997..2001
FT		/*tag= j
FT		/function= Related with mRNA instability
FT	misc_feature	2119..2123
FT		/*tag= k
FT		/function= Related with mRNA instability
FT	misc_feature	2273..2277
FT		/*tag= l
FT		/function= Related with mRNA instability
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FT		/*tag= n
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FT	misc_feature	3484..3488
FT		/*tag= o
FT		/function= Related with mRNA instability
FT	misc_feature	3495..3499

FT /*tag= p
 FT /function= Related with mRNA instability
 FT misc_feature 3632..3636
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 FT misc_feature 3852..3856
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 FT /*tag= s
 FT /function= Related with mRNA instability
 FT misc_feature 4213..4217
 FT /*tag= t
 FT /function= Related with mRNA instability

XX

PN EP522868-A1.

XX

PD 13-JAN-1993.

XX

PF 10-JUL-1992; 92EP-0306347.

XX

PR 12-JUL-1991; 91JP-0172828.

XX

PA (SHIO) SHIONOGI SEIYAKU KK.

XX

PI Imura H, Nakanishi S, Nakao K;

XX

DR WPI; 1993-010677/02.

DR P-PSDB; AAR30886.

XX

PT Human ETa and ETb endothelin receptors - for measuring endothelin
 PT and screening for endothelin antagonists

XX

PS Claim 12; Fig 2; 39pp; English.

XX

CC The sequences given in AAQ34583-84 encode the human ETa and ETb
 CC endothelin receptors respectively. ETa is a 427 amino acid protein
 CC with a molecular weight of 48,726. ETb comprises 442 amino acids and
 CC has a molecular weight of 49,629. ETa has a higher affinity for
 CC endothelin (ET)-1 and ET-2, whereas ETb has no selectivity for ET-1,
 CC ET-2 or ET-3. The receptors each contain seven transmembrane domains
 CC and have an extracellular N tail and a cytoplasmic C tail. There are
 CC several potential sites for post translational modification, these
 CC sites are identical to those of bovine ET-1 receptor. ETa cDNA is
 CC 91.2% homologous to bovine ET-1 receptor cDNA and ETb cDNA is 61.1%
 CC homologous to that of bovine ETa-receptor. The receptor proteins are
 CC useful as reagents for measuring the amount of ET or screening for
 CC antagonists of the ET receptor when studying the circulatory system.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 4301 BP; 1342 A; 830 C; 815 G; 1314 T; 0 other;

Query Match 99.9%; Score 4297.8; DB 14; Length 4301;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4299; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGACATTCCGGTGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Db	1	 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Db	241	 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	 CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Db	541	 TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900

Db	841	GCTGTTGCTTCTTGGAGTAGAATTTAAAGGAATTGGGGTTCCAAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTTGAT	960
Db	901	ATTGTTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTACTCACAGCTACATATGACATTTTATGAGCTGT	1740

Qy	1741	TTACGGCATGGAAAAGAAAAATCAGTGGGAATTAAGAAAAGCCTCGTCGTGAAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAAGAAAAATCAGTGGGAATTAAGAAAAGCCTCGTCGTGAAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAAACAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAAACAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580

Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCACTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCACTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAACCTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAACCTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCAGGTTTATTAA	3480

Db	3421	 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	 TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT	3660
Db	3601	 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	 CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	4200
Db	4141	 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301	

Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAA 4301

RESULT 2

AAF21284

ID AAF21284 standard; DNA; 4286 BP.

XX

AC AAF21284;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide related sequence #2851.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

XX

PD 26-OCT-2000.

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PF 24-MAR-2000; 2000WO-US08020.

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PR 06-APR-1999; 99US-0127958.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -

XX

PS Disclosure; Page 1273-1274; 1592pp; English.

XX

CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and

Qy	481	CCACGCACCATCTCCCTCCCTCCCTGCCAAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCTCCCTCCCTGCCAAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTCCTGCCCTTGTGTTCTGCTGCGGATCATCGGGAACCTCCACA	600
Db	541	TACATCAACACGGTTGTGTCTCCTGCCCTTGTGTTCTGCTGCGGATCATCGGGAACCTCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTGTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTGTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTCAAGTTTCTAT	1080
Db	1021	AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTCAAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320

Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATCTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATCTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACTCTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTAAGTGTAATTATTTTAACTCTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTCACTAGAAGCCCAACCTCAGCATTCTGCAATATGTAAC	2220

Db	2161	 TTTTGAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	 GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060

Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT	3900

Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

RESULT 3

AAA35162

ID AAA35162 standard; DNA; 4286 BP.

XX

AC AAA35162;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:36.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020

Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTCGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTCGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC TGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAC TGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCCTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCCTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATTACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATTACACAACACT	1860

Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTGTGTCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTGTGTCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760

Db	2701	 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Db	3001	 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Qy	3061	CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	 CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACATGTGGCCA	3300
Db	3241	 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	 GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	 ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Db	3481	 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600

Db	3541	TCCTGATACCCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

RESULT 4

ABV94186

ID ABV94186 standard; cDNA; 4286 BP.

XX

AC ABV94186;

XX

DT 08-JAN-2003 (first entry)
XX
DE Breast carcinoma related nucleotide sequence SEQ ID NO:177.
XX
KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200246467-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-IB02811.
XX
PR 08-DEC-2000; 2000US-254090P.
PR 07-DEC-2001; 2001US-0007926.
XX
PA (IPSO-) IPSOGEN.
XX
PI Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
XX
DR WPI; 2002-619023/66.
XX
PT Novel polynucleotide library useful in molecular characterization of a
PT carcinoma, comprising a pool of polynucleotide sequences or its
PT subsequences which are either underexpressed or overexpressed in tumor
PT cells -
XX
PS Claim 1; Page 225-226; 401pp; English.
XX
CC The present invention describes a polynucleotide library (I) useful in
CC the molecular characterisation of a carcinoma, comprising a pool of
CC polynucleotides or its subsequences which are either underexpressed or
CC overexpressed in tumour cells, and correspond to any of the
CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
CC (M1) differentially expressed polynucleotide sequences which are
CC correlated with a cancer, involves obtaining a polynucleotide sample from
CC a patient, and reacting the polynucleotide sample obtained with a probe
CC immobilised on a solid support, where the probe comprises any combination
CC of the polynucleotide sequences of (I) or its expression products encoded
CC by polynucleotide sequences of (I), and detecting the reaction product.
CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
CC useful for the prognosis or diagnostic of tumour, in differentiating a
CC normal cell from a cancer cell, detecting a hormone sensitive tumour
CC cell, differentiating a tumour with lymph nodes from a tumour without
CC lymph nodes, differentiating antracycline-sensitive tumours from
CC antracycline-insensitive tumours, and classifying good and poor prognosis
CC primary breast tumours. (I) is useful for large-scale molecular
CC characterisation of breast cancer that help in prediction, prognosis and
CC cancer treatment, and for detecting differentially expressed genes that
CC correlated with a cancer.
XX
SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 other;

Query Match 99.6%; Score 4284.4; DB 24; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780

Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTTGCAATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTTGCAATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680

Db	1621	 AACAAAATGAAACATTTGCCAAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	 TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT	1860
Db	1801	 TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Db	1861	 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAAACAGAACTTTTAAATG	1980
Db	1921	 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATAT	2040
Db	1981	 AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATAT	2040
Qy	2041	TATCACAATATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	 TATCACAATATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	 TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTC	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTC	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAACTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAACTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGTCATCTGTAAATACTTACCTACATACA	2520

Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCTGTATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCTGTATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360

Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTACTGCTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCAGAGTTTATTAA	3480
Db	3421	CATTTTACTGCTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCAGAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA	3540
Db	3481	TATATTTAATTTCTATTTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAATCATGGATGTTA	3840
Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAATCATGGATGTTA	3840
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAAACCAATAAAAAATTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
 ||||||||||||||||||||||||
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 5

ABZ42661

ID ABZ42661 standard; DNA; 4286 BP.

XX

AC ABZ42661;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human endothelin B receptor nucleotide SEQ ID NO:113.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US50107.

XX

PR 19-DEC-2000; 2000US-257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR

P-PSDB; ABP81815.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising:

CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino

CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 other;

Query Match 99.6%; Score 4284.4; DB 25; Length 4286;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420

Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTTGTGCTTGTGCTGCTGGGGATCATCGGGAACTCCACA	600
Db	541	TACATCAACACGGTTGTGTCTTGTGCTTGTGCTGCTGGGGATCATCGGGAACTCCACA	600
Qy	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCACCTC	1260

Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160

Db	2101	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	 TTTTGAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	 CAACATGTCAAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	2281	 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTC	2400
Db	2341	 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTC	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	 GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	 GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCTCTAGAGGCAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTCTCTAGAGGCAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000

Db	2941	GGGATGAGATGTGTGTGTAAGATATGTACAAGAGAAAACCGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCCAAACCAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCCAAACCAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTAGTGGCTT	3660
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840

Qy	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	3841	CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Qy	3961	GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	3961	GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Qy	4081	TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	4081	TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286
Db	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

RESULT 6

AAF21288

ID AAF21288 standard; DNA; 13611 BP.

XX

AC AAF21288;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide related sequence #2855.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 1277-1280; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 13611 BP; 3676 A; 3007 C; 3056 G; 3868 T; 4 other;

 Query Match 99.6%; Score 4284.4; DB 21; Length 13611;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
 |||
 Db 1873 GAGACATTCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 1932

Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
 |||
 Db 1933 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 1992

Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
 |||
 Db 1993 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 2052

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
 |||
 Db 2053 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 2112

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
 |||
 Db 2113 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 2172

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
 |||
 Db 2173 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 2232

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
 |||
 Db 2233 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 2292

Qy 421 CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
 |||
 Db 2293 CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 2352

Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 540
 |||
 Db 2353 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 2412

Qy 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA 600
 |||
 Db 2413 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA 2472

Qy 601 CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
 |||
 Db 2473 CTTCTGAGAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 2532

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
 |||
 Db 2533 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 2592

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780
 |||
 Db 2593 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 2652

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840
 |||
 Db 2653 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 2712

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Db	2713	 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	2772
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	2773	 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	2832
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	2833	 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	2892
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	2893	 AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	2952
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	2953	 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	3012
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	3013	 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	3072
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	3073	 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC	3132
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	3133	 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	3192
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	3193	 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	3252
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	3253	 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	3312
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	3313	 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	3372
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	3373	 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	3432
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	3433	 TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAA	3492
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	3493	 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	3552
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	1740

Db	3553	TAAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT	3612
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	3613	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	3672
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	3673	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	3732
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	3733	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	3792
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	1980
Db	3793	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG	3852
Qy	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT	2040
Db	3853	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT	3912
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	3913	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	3972
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	3973	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	4032
Qy	2161	TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	4033	TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	4092
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	4093	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	4152
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	4153	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	4212
Qy	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	4213	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	4272
Qy	2401	CATACCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	4273	CATACCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	4332
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	4333	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	4392
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	4393	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	4452

Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	4453		
Qy	2641	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	4512
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT	2700
Db	4513		
Qy	2641	GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT	4572
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	4573		
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	4632
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	4633		
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	4692
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Db	4693		
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	4752
Qy	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	4753		
Qy	2881	AGCTTTGTGCGTTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	4812
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	4813		
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	4872
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	4873		
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	4932
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	4933		
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	4992
Qy	3121	GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	4993		
Qy	3121	GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	5052
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	5053		
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	5112
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	5113		
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	5172
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Db	5173		
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	5232
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	5233		
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	5292

Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	5293	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	5352
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Db	5353	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	5412
Qy	3541	TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	5413	TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	5472
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT	3660
Db	5473	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT	5532
Qy	3661	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	5533	TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	5592
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	5593	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	5652
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
Db	5653	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	5712
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	5713	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	5772
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	5773	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	5832
Qy	3961	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	4020
Db	5833	GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT	5892
Qy	4021	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	4080
Db	5893	AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT	5952
Qy	4081	TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	4140
Db	5953	TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC	6012
Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	4200
Db	6013	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA	6072
Qy	4201	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	4260
Db	6073	CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT	6132
Qy	4261	AAAATGCCACATTTCTGGTCTCTGGG	4286

Db 6133 AAAATGCCACATTTCTGGTCTCTGGG 6158

RESULT 7

AAA35166

ID AAA35166 standard; DNA; 13612 BP.

XX

AC AAA35166;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:40.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

PI Nyce JW;

XX

DR WPI; 2000-205971/18.

XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

XX

PS Disclosure; Page 1194-1197; 1343pp; English.

XX

CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	600
Db	2413	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA	2472
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	2473	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	2532
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	2533	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	2592
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	2593	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	2652
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	2653	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	2712
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	2713	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	2772
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	2773	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	2832
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	2833	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	2892
Qy	1021	AAGACAGCTTTCATGTCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	2893	AAGACAGCTTTCATGTCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	2952
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	2953	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	3012
Qy	1141	AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	3013	AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	3072
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCACCTC	1260
Db	3073	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTTCACCTC	3132
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	3133	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	3192
Qy	1321	AGCTTCTGTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	3193	AGCTTCTGTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	3252
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440

Db	3253	 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	3312
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	3313	 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	3372
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	3373	 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	3432
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	3433	 TCTTGAAAGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAA	3492
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGTATGTATTTGCACAGCACACTAT	1680
Db	3493	 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAAGTATGTATTTGCACAGCACACTAT	3552
Qy	1681	TAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	3553	 TAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	3612
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	3613	 TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	3672
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	3673	 TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	3732
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	3733	 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	3792
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	3793	 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	3852
Qy	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTTTCAATTAATAT	2040
Db	3853	 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTTTCAATTAATAT	3912
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	3913	 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	3972
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	3973	 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	4032
Qy	2161	TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	4033	 TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	4092
Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280

Db	4093	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	4152
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	2340
Db	4153	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA	4212
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	4213	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	4272
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	4273	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT	4332
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	2520
Db	4333	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA	4392
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	4393	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	4452
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	4453	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	4512
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	4513	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	4572
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	2760
Db	4573	GCTATAGTTAAAATACTATTTTTTCAAATCATAAGATTAGTACATTTAACAGCTACCTG	4632
Qy	2761	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	4633	TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	4692
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	2880
Db	4693	ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT	4752
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	4753	AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	4812
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	4813	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	4872
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	4873	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT	4932
Qy	3061	CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	4933	CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	4992

Qy	3121	GAGTGACTTTTCGAAATAAAATTGGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	3180
Db	4993	GAGTGACTTTTCGAAATAAAATTGGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA	5052
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	5053	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	5112
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	5113	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	5172
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Db	5173	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	5232
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	5233	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	5292
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCACAGTTTATTAA	3480
Db	5293	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCACAGTTTATTAA	5352
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Db	5353	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	5412
Qy	3541	TCCTGATACCCTTTCTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	5413	TCCTGATACCCTTTCTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	5472
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	3660
Db	5473	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT	5532
Qy	3661	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	3720
Db	5533	TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT	5592
Qy	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
Db	5593	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	5652
Qy	3781	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAACATGGATGTTA	3840
Db	5653	TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAACATGGATGTTA	5712
Qy	3841	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
Db	5713	CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	5772
Qy	3901	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	3960
Db	5773	GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA	5832

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Qy      3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5833 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 5892

Qy      4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5893 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 5952

Qy      4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5953 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 6012

Qy      4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6013 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 6072

Qy      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6073 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 6132

Qy      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
          ||||||||||||||||||||||||
Db      6133 AAAATGCCACATTTCTGGTCTCTGGG 6158

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RESULT 8

ABK94410

ID ABK94410 standard; DNA; 2972 BP.

XX

AC ABK94410;

XX

DT 27-AUG-2002 (first entry)

XX

DE DNA encoding endothelin receptor B (EDNRB), exon 7.

XX

KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRB;
KW endothelin receptor B; signaling system; cardiovascular disease;
KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;
KW fatty acid metabolism; diabetes; familial hypercholesterolaemia;
KW forensic marker; transgenic animal; solid support; SNP;
KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	variation	replace(1048,A)
FT		/*tag= a
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(1658,C)
FT		/*tag= b
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(1912,T)
FT		/*tag= c
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(2130,T)
FT		/*tag= d
FT		/standard_name= "Single nucleotide polymorphism"

XX
 PN WO200224747-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-EP10087.
 XX
 PR 19-SEP-2000; 2000EP-0120123.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Brinkmann U, Hoffmeyer S;
 XX
 DR WPI; 2002-435060/46.
 XX
 PT Novel polynucleotide of the endothelin/endothelin converting
 PT enzyme/receptors of endothelin and endothelin converting enzyme
 PT signaling system associated with cardiovascular disease, useful for
 PT treating the disease -
 XX
 PS Claim 1; Page -; 190pp; English.
 XX
 CC The invention describes a polynucleotide (I) of the endothelin
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 CC signaling system which is associated with a cardiovascular disease. (I),
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
 CC or (II) is useful for producing cells capable of expressing a molecular
 CC variant polypeptide which is associated with a cardiovascular disease.
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
 CC a molecular variant gene comprising (I) is useful for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
 CC or its gene product, or for identifying and obtaining an inhibitor of
 CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
 CC signaling system or its gene product. The isolated proteins and
 CC polynucleotides encoding them are useful for preparation of a
 CC pharmaceutical composition for treating a cardiovascular disease such as
 CC coronary heart disease, hypertension, atherosclerosis, or related to
 CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
 CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
 CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
 CC creating a transgenic animal and in creation of a solid support
 CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
 CC host cells of the invention. This sequence encodes a fragment of the
 CC cardioavascular regulator Endothelin receptor B (EDNRB).
 CC Note: This sequence does not appear in the specification but has been
 CC obtained from GenBank using information given in the invention.
 XX
 SQ Sequence 2972 BP; 1018 A; 499 C; 465 G; 990 T; 0 other;

Query Match 66.4%; Score 2857; DB 24; Length 2972;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2857; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 9 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 68

Qy	1490	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	1549
Db	69	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	128
Qy	1550	AATACAGCTCATCTTGAAAGAAGAACTATTCACCTGTATTTCATTTTCTTTATATTGGACC	1609
Db	129	AATACAGCTCATCTTGAAAGAAGAACTATTCACCTGTATTTCATTTTCTTTATATTGGACC	188
Qy	1610	GAAGTCATTAAAAACAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA	1669
Db	189	GAAGTCATTAAAAACAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA	248
Qy	1670	CAGCACACTATTAAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATT	1729
Db	249	CAGCACACTATTAAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATT	308
Qy	1730	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	1789
Db	309	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	368
Qy	1790	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATT	1849
Db	369	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATT	428
Qy	1850	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	1909
Db	429	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	488
Qy	1910	ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	1969
Db	489	ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	548
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT	2029
Db	549	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT	608
Qy	2030	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	2089
Db	609	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	668
Qy	2090	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	2149
Db	669	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	728
Qy	2150	AGCAAGGCTGTTTTTGAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	2209
Db	729	AGCAAGGCTGTTTTTGAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	788
Qy	2210	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	789	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	848
Qy	2270	TGAATTTAAATATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTCACTTAAG	2329
Db	849	TGAATTTAAATATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTCACTTAAG	908

Qy	2330	ATCAAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTGAA	2389
Db	909	ATCAAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAAGACTTTTTTGAA	968
Qy	2390	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	2449
Db	969	TCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	1028
Qy	2450	ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	1029	ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	1088
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	1089	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	1148
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	2629
Db	1149	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	1208
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGC	2689
Db	1209	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGC	1268
Qy	2690	ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	2749
Db	1269	ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA	1328
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	1329	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	1388
Qy	2810	AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	2869
Db	1389	AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	1448
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT	2929
Db	1449	AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT	1508
Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	2989
Db	1509	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	1568
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	3049
Db	1569	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	1628
Qy	3050	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	3109
Db	1629	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	1688
Qy	3110	CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	1689	CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	1748
Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	3229

Db	1749	 AATATGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	1808
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	3289
Db	1809	 AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	1868
Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
Db	1869	 CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	1928
Qy	3350	ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	1929	 ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	1988
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCA	3469
Db	1989	 ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCA	2048
Qy	3470	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	3529
Db	2049	 CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	2108
Qy	3530	GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	2109	 GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	2168
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	3649
Db	2169	 TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	2228
Qy	3650	TTCAGTGGCTTTTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	3709
Db	2229	 TTCAGTGGCTTTTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA	2288
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	2289	 ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	2348
Qy	3770	TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	3829
Db	2349	 TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	2408
Qy	3830	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	3889
Db	2409	 CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	2468
Qy	3890	CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	2469	 CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	2528
Qy	3950	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	2529	 AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	2588
Qy	4010	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069

Db 2589 TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCCTAAAGTGGCTATA 2648
 Qy 4070 GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACATA 4129
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2649 GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACATA 2708
 Qy 4130 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2709 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 2768
 Qy 4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 4249
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2769 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 2828
 Qy 4250 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2829 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 2865

RESULT 9

ABQ77402/c

ID ABQ77402 standard; DNA; 183337 BP.

XX

AC ABQ77402;

XX

DT 10-MAY-2003 (first entry)

XX

DE Human EDNRB DNA.

XX

KW Human; EDNRB; vascular disease; cardiant; antiarteriosclerotic; stroke;
 KW cerebroprotective; gene therapy; coronary artery disease; ischaemia;
 KW myocardial infarction; peripheral vascular disease; pulmonary embolism;
 KW venous thromboembolism; forensic; paternity testing; GI12597038; gene;
 KW SNP; single nucleotide polymorphism; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT variation replace (75672,t)

FT /*tag= a

FT /standard_name= "SNP"

FT /note= "Single nucleotide polymorphism (ID G337a4)

FT which does not change the EDNBR protein"

XX

PN WO2003016494-A2.

XX

PD 27-FEB-2003.

XX

PF 16-AUG-2002; 2002WO-US26343.

XX

PR 16-AUG-2001; 2001US-313097P.

PR 05-OCT-2001; 2001US-327485P.

PR 14-DEC-2001; 2001US-0020141.

XX

PA (VITI-) VITIVITY INC.

XX

PI McCarthy J, Ableson A;

XX
DR WPI; 2003-300617/29.
DR P-PSDB; ABG74670.
XX
PT Identifying a subject as a candidate for a particular course of therapy
PT to treat a vascular disease or disorder, e.g. stroke, myocardial
PT infarction or ischemia by determining the identity of the nucleotide
PT present at specific positions -
XX
PS Claim 1; Fig 5; 568pp; English.
XX
CC This invention describes a novel method for identifying a subject as a
CC candidate for a particular course of therapy to treat a vascular disease
CC or disorder. The method comprises determining the identity of the
CC nucleotide present at specific positions, or their complements, and
CC identifying the subject as a candidate for a particular clinical course
CC of therapy based on the identity of the nucleotide present in that
CC specific position. The method can be used for identifying a subject who
CC is a candidate for further diagnostic evaluation of a vascular disease or
CC disorder and selecting a clinical course of therapy. The products of the
CC invention have cardiant, antiarteriosclerotic and cerebroprotective
CC activity and can be used for gene therapy. The methods disclosed are
CC useful for treating a vascular disease, e.g. atherosclerosis, coronary
CC artery disease, myocardial infarction, ischaemia, stroke, peripheral
CC vascular diseases, venous thromboembolism and pulmonary embolism. The DNA
CC sequences are useful as fingerprint for detecting different individuals
CC within the same species applicable in forensic studies and paternity
CC testing. This sequence encodes the human EDNBR gene represented in
CC GI12597038, used to illustrate the method of the invention.
XX
SQ Sequence 183337 BP; 56451 A; 33595 C; 34663 G; 58628 T; 0 other;

Query Match 66.1%; Score 2841.8; DB 25; Length 183337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2854; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	1430	AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC	1489
Db	72830	AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC	72771
Qy	1490	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	1549
Db	72770	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	72711
Qy	1550	AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC	1609
Db	72710	AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC	72651
Qy	1610	GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAAACAAAAACAAAAAATATGTATTTGCA	1669
Db	72650	GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAAACAAAAACAAAAAATATGTATTTGCA	72591
Qy	1670	CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT	1729
Db	72590	CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT	72531
Qy	1730	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	1789

Db	72530	 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	72471
Qy	1790	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	1849
Db	72470	 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	72411
Qy	1850	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	1909
Db	72410	 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG	72351
Qy	1910	ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	1969
Db	72350	 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA	72291
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT	2029
Db	72290	 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT	72231
Qy	2030	TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	2089
Db	72230	 TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT	72171
Qy	2090	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	2149
Db	72170	 AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG	72111
Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	2209
Db	72110	 AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTG	72051
Qy	2210	CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	72050	 CAATATGTAACCAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	71991
Qy	2270	TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAG	2329
Db	71990	 TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAG	71931
Qy	2330	ATCAAACCTCACAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	2389
Db	71930	 ATCAAACCTCACAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	71871
Qy	2390	TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	2449
Db	71870	 TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	71811
Qy	2450	ATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	71810	 ATCTTCTTCTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	71751
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	71750	 ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	71691
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	2629

Db	71690	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	71631
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	2689
Db	71630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC	71571
Qy	2690	ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAATCATAACAGATTAGTACATTTA	2749
Db	71570	ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAATCATAACAGATTAGTACATTTA	71511
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
Db	71510	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	71451
Qy	2810	AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	2869
Db	71450	AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	71391
Qy	2870	AAGAACCCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	2929
Db	71390	AAGAACCCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	71331
Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	2989
Db	71330	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	71271
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	3049
Db	71270	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTT	71211
Qy	3050	CGTCATTGCCTCGTCCATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTG	3109
Db	71210	CGTCATTGCCTCGTCCATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTG	71151
Qy	3110	CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	71150	CAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	71091
Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGGCCACATGTTGGAAATA	3229
Db	71090	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGGCCACATGTTGGAAATA	71031
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	3289
Db	71030	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	70971
Qy	3290	CAATGTGGCCAGAAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
Db	70970	CAATGTGGCCAGAAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	70911
Qy	3350	ATAAATCACCCACAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
Db	70910	ATAAATCACCCACAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	70851
Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
Db	70850	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	70791

Qy	3470	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT	3529
Db	70790	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT	70731
Qy	3530	GAATTTTACATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	70730	GAATTTTACATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATC	70671
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	3649
Db	70670	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCA	70611
Qy	3650	TTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	3709
Db	70610	TTCAGTGGCTTTTT-AAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	70552
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACT	3769
Db	70551	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACT	70492
Qy	3770	TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	3829
Db	70491	TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	70432
Qy	3830	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTAT	3889
Db	70431	CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTAT	70372
Qy	3890	CCACTGCTAATGTGGATGTATGTTCAAAACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	70371	CCACTGCTAATGTGGATGTATGTTCAAAACCTTTTAGTATTGATAGCTTACATATGGCC	70312
Qy	3950	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	70311	AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	70252
Qy	4010	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069
Db	70251	TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	70192
Qy	4070	GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTA	4129
Db	70191	GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTA	70132
Qy	4130	CCTTATTTTTCTACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA	4189
Db	70131	CCTTATTTTTCTACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA	70072
Qy	4190	TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	4249
Db	70071	TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA	70012
Qy	4250	GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	4286
Db	70011	GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	69975

AAV17875

```
Query Match          39.3%;   Score 1691.8;   DB 19;   Length 1873;
Best Local Similarity 99.6%;   Pred. No. 0;
Matches 1696;   Conservative      0;   Mismatches      7;   Indels      0;   Gaps      0;

Qy      178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
        ||    || ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||
Db      171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy      238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGC 297
        ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||
Db      231 ATGCAGCCGCCTCCAAGTCTGTGCGGACCGGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGC 290
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Qy	298	CTGTTCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	357
Db	291	CTGTTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	350
Qy	358	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	417
Db	351	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	410
Qy	418	AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	477
Db	411	AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	537
Db	471	CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	530
Qy	538	AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACTCC	597
Db	531	AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACTCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130

Qy	1138	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGCTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGCTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGTC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGTC	1370
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1437
Db	1371	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAAAACAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1677
Db	1611	TAAAAACAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	TATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1730
Qy	1738	TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1797
Db	1731	TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAAC	1857
Db	1791	AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAAC	1850
Qy	1858	ACTTAGGCTTAAAAATGAGCTCA	1880
Db	1851	ACTTAGGCTTAAAAATGAGCTCA	1873

RESULT 11

ID AAF21283 standard; DNA; 1872 BP.

XX

AC AAF21283;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide related sequence #2850.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 1273; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The

Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCTGGTCCCTTGCTTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCTGGTCCCTTGCTTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370
Qy	1378	ATTAACCCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGTCTTTAAGTCATGC	1437
Db	1371	ATTAACCCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGTCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1610

Qy 1618 TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1677
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1611 TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1670
 Qy 1678 TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1737
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1671 TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1730
 Qy 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790
 Qy 1798 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1857
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1791 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1850
 Qy 1858 ACTTAGGCTTAAAAATGAGCTC 1879
 ||||||||||||||||||
 Db 1851 ACTTAGGCTTAAAAATGAGCTC 1872

RESULT 12

AAA35161

ID AAA35161 standard; DNA; 1872 BP.

XX

AC AAA35161;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:35.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

PI Nyce JW;

XX

DR WPI; 2000-205971/18.

XX

Db	411	AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTC	537
Db	471	CCGCCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTC	530
Qy	538	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACTCC	597
Db	531	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACTCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAAGTGATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAAGTGATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAAATGATCCCAATAGATGTGAACTT	1310

Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1437
Db	1371	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACAC	1677
Db	1611	TAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1730
Qy	1738	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1797
Db	1731	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1857
Db	1791	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1850
Qy	1858	ACTTAGGCTTAAAAATGAGCTC	1879
Db	1851	ACTTAGGCTTAAAAATGAGCTC	1872

RESULT 13

AAF21285

ID AAF21285 standard; DNA; 1719 BP.

XX

AC AAF21285;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide related sequence #2852.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;

KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 1274-1275; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of

CC the present invention.

XX

SQ Sequence 1719 BP; 444 A; 400 C; 412 G; 463 T; 0 other;

Query Match 34.8%; Score 1495.4; DB 21; Length 1719;
Best Local Similarity 99.8%; Pred. No. 2.5e-303;
Matches 1503; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	203	GCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG	262
Db	200	GCGGCCACCGGACG-CTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG	258
Qy	263	GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGGGGAGAGGAGA	322
Db	259	GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGGGGAGAGGAGA	318
Qy	323	GAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC	382
Db	319	GAGGCTTCCCGCCCGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC	378
Qy	383	CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTGCTTGGCACCTG	442
Db	379	CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTGCTTGGCACCTG	438
Qy	443	CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC	502
Db	439	CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC	498
Qy	503	CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCT	562
Db	499	CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTCT	558
Qy	563	GCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA	622
Db	559	GCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA	618
Qy	623	ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC	682
Db	619	ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC	678
Qy	683	TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT	742
Db	679	TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT	738
Qy	743	TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG	802
Db	739	TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG	798
Qy	803	TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA	862
Db	799	TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA	858
Qy	863	TTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAATTGTTTTGATTGGGTGGTCT	922
Db	859	TTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAATTGTTTTGATTGGGTGGTCT	918
Qy	923	CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTTGATATAATTACGATGGACTACAAAG	982

Db	919		CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG	978
Qy	983		GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTTCATGCAGTTTT	1042
Db	979		GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTTCATGCAGTTTT	1038
Qy	1043		ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1102
Db	1039		ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1098
Qy	1103		CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1162
Db	1099		CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1158
Qy	1163		TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1222
Db	1159		TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1218
Qy	1223		TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1282
Db	1219		TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1278
Qy	1283		TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1342
Db	1279		TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1338
Qy	1343		ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1402
Db	1339		ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1398
Qy	1403		TGAGCAAAAGATTCAAAAACGCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1462
Db	1399		TGAGCAAAAGATTCAAAAACGCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1458
Qy	1463		AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1522
Db	1459		AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1518
Qy	1523		GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1582
Db	1519		GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1578
Qy	1583		TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAAACATTTGCCAA	1642
Db	1579		TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAAACATTTGCCAA	1638
Qy	1643		AACAAAACAAAAACTATGTATTTGCACAGCACACTATTAAATATTAAGTGTAATTATT	1702
Db	1639		AACAAAACAAAAACTATGTATTTGCACAGCACACTATTAAATATTAAGTGTAATTATT	1698
Qy	1703		TTAACA 1708	
Db	1699		TTAAAA 1704	

AAA35163

ID AAA35163 standard; DNA; 1720 BP.

XX

AC AAA35163;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:37.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

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PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

XX

PI Nyce JW;

XX

DR WPI; 2000-205971/18.

XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

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PS Disclosure; Page 1192; 1343pp; English.

XX

CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing

Db	799	 TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA	858
Qy	863	TTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCT	922
Db	859	 TTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCT	918
Qy	923	CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG	982
Db	919	 CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG	978
Qy	983	GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT	1042
Db	979	 GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT	1038
Qy	1043	ACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1102
Db	1039	 ACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA	1098
Qy	1103	CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1162
Db	1099	 CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGA	1158
Qy	1163	TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1222
Db	1159	 TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG	1218
Qy	1223	TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1282
Db	1219	 TCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC	1278
Qy	1283	TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1342
Db	1279	 TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT	1338
Qy	1343	ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1402
Db	1339	 ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG	1398
Qy	1403	TGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1462
Db	1399	 TGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTG	1458
Qy	1463	AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1522
Db	1459	 AAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACG	1518
Qy	1523	GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1582
Db	1519	 GATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAAGAACTATTAC	1578
Qy	1583	TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAACAAAATGAAACATTTGCCAA	1642
Db	1579	 TGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAACAAAATGAAACATTTGCCAA	1638
Qy	1643	AACAAAACAAAAAATATGTATTTGCACAGCACACTATTAAAATATTAAGTGTAATTATT	1702

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Db      1639 AACAAAACAAAAAACTATGTATTTGCACAGCACACTATTAAATATTAAGTGTATTATT 1698
Qy      1703 TTAACA 1708
        |||||
Db      1699 TTAAAA 1704

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RESULT 15

ACA56605

ID ACA56605 standard; cDNA; 1470 BP.

XX

AC ACA56605;

XX

DT 06-JUN-2003 (first entry)

XX

DE Human signalling pathway polynucleotide probe SEQ ID NO 1203.

XX

KW Human; probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX

OS Homo sapiens.

XX

PN US6500938-B1.

XX

PD 31-DEC-2002.

XX

PF 30-JAN-1998; 98US-0016434.

XX

PR 30-JAN-1998; 98US-0016434.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Au-Young J, Seilhamer JJ;

XX

DR WPI; 2003-352189/33.

XX

PT Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

PT polynucleotides -

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PS Claim 1; SEQ ID NO 1203; 65pp; English.

XX

CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding

CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.

XX

SQ Sequence 1470 BP; 381 A; 343 C; 350 G; 396 T; 0 other;

Query Match 34.1%; Score 1466.8; DB 25; Length 1470;
Best Local Similarity 99.9%; Pred. No. 2.3e-297;
Matches 1468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	192	GAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC	251
Db	1	GAAACTGCGGACGGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC	60
Qy	252	AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTG	311
Db	61	AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTG	120
Qy	312	GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT	371
Db	121	GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT	180
Qy	372	AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC	431
Db	181	AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC	240
Qy	432	GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT	491
Db	241	GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT	300
Qy	492	CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC	551
Db	301	CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC	360
Qy	552	GGTTGTGTCTGCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT	611
Db	361	GGTTGTGTCTGCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT	420
Qy	612	TATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT	671
Db	421	TATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT	480
Qy	672	GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA	731
Db	481	GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA	540
Qy	732	GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT	791
Db	541	GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT	600
Qy	792	GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC	851

Db	601	GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC	660
Qy	852	TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAATTGTTTTGAT	911
Db	661	TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAATTGTTTTGAT	720
Qy	912	TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	971
Db	721	TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT	780
Qy	972	GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	1031
Db	781	GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT	840
Qy	1032	CATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTTCTATTTCTGCTTGCC	1091
Db	841	CATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTTCTATTTCTGCTTGCC	900
Qy	1092	ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAAGAAAAG	1151
Db	901	ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAAGAAAAG	960
Qy	1152	TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT	1211
Db	961	TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT	1020
Qy	1212	CTTTTGCCTGGTCCCTTGCTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT	1271
Db	1021	CTTTTGCCTGGTCCCTTGCTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT	1080
Qy	1272	GAAGCTCACTCTTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT	1331
Db	1081	GAAGCTCACTCTTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT	1140
Qy	1332	GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC	1391
Db	1141	GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC	1200
Qy	1392	TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG	1451
Db	1201	TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG	1260
Qy	1452	CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAAGCAGTCGTGCTTAAAGTTCAAAGC	1511
Db	1261	CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAAGCAGTCGTGCTTAAAGTTCAAAGC	1320
Qy	1512	TAATGATCACGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA	1571
Db	1321	TAATGATCACGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA	1380
Qy	1572	GAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAAATGAA	1631
Db	1381	GAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAAATGAA	1440
Qy	1632	ACATTTGCCAAAAACAAAAACAAAAACTATG	1661
Db	1441	ACATTTGCCAAAAACAAAAACAAAAACTATG	1470

Search completed: December 12, 2003, 11:27:19
Job time : 1006.18 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:16:57 ; Search time 15090.3 Seconds
(without alignments)
11659.930 Million cell updates/sec

Title: US-09-931-157-2
Perfect score: 4301
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
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14: gb_vi:*
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17: em_hum:*
18: em_in:*
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21: em_or:*
22: em_ov:*
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 37: em_htg_vrt:*
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 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
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	1	4301	100.0	4301	6	AR177880 Sequence
	2	4301	100.0	4301	6	E07650 cDNA encodi
	3	4286	99.7	4286	9	HUMETR D90402 Homo sapien
	4	4284.4	99.6	4286	6	AX548828 Sequence
	5	4284.4	99.6	4286	6	AX587707 Sequence
	6	4284.4	99.6	4286	9	S57283 Homo sapien
	7	2857	66.4	2972	9	D13162S7 Homo sapien
c	8	2841.8	66.1	183337	9	AL139002 Human DNA
c	9	2792.4	64.9	201093	2	AC144750 Pan trogl
	10	2610	60.7	2720	11	G06417 human STS W
c	11	2550	59.3	169751	2	AC130785 Papio anu
c	12	2550	59.3	185870	2	AC129069 Papio anu
	13	1691.8	39.3	1873	6	AR165435 Sequence
	14	1691.8	39.3	1873	6	E15242 Human mRNA
	15	1690.8	39.3	1872	9	S44866 ETB endothe
	16	1495.4	34.8	1719	9	HUMEDNRB L06623 Homo sapien
	17	1466.8	34.1	1470	6	AR270640 Sequence
	18	1466.8	34.1	1470	9	HUMETSR M74921 Human endot
	19	1389	32.3	1603	9	BC014472 Homo sapi
	20	1389	32.3	1632	6	AX342673 Sequence
	21	1361.4	31.7	1765	9	AF114165 Homo sapi
	22	1327.4	30.9	1329	9	AY275463 Homo sapi
	23	1322.6	30.8	1329	6	AX280873 Sequence
	24	1222.8	28.4	1669	4	AF019072 Equus cab
	25	1220.4	28.4	1578	9	HSX99250 H.sapiens m
	26	1197.8	27.8	2026	4	BOVEETBR D90456 Bos taurus
	27	1186	27.6	1452	4	AF034530 Canis fam
	28	1113	25.9	2018	10	S65355 nonselectiv
	29	1110.2	25.8	1551	6	E05930 DNA sequenc
	30	1104.8	25.7	2115	10	BC026553 Mus muscu
	31	1099.2	25.6	1958	6	AX305434 Sequence
	32	1099.2	25.6	1958	10	MMU32329 Mus musculu
	33	1091	25.4	1892	10	RNETBREC X57764 Rat mRNA fo

34	1091	25.4	1965	6	E03623	E03623 DNA encodin
35	1086.6	25.3	1311	4	AF038900	AF038900 Equus cab
36	1070.4	24.9	1321	6	AR207426	AR207426 Sequence
37	1067.6	24.8	1314	4	AF276427	AF276427 Canis fam
38	1042.8	24.2	1326	4	AF245469	AF245469 Oryctolag
c 39	931.8	21.7	135327	2	AC118537	AC118537 Felis cat
c 40	931.8	21.7	170121	2	AC123546	AC123546 Felis cat
c 41	922.2	21.4	192330	2	AC122157	AC122157 Canis fam
42	746	17.3	1564	5	AF472616	AF472616 Gallus ga
43	732.6	17.0	1041	5	CCEDNRB	X99295 C.coturnix
44	588	13.7	588	11	G15922	G15922 human STS C
45	564.8	13.1	1520	5	AF275636	AF275636 Danio rer

ALIGNMENTS

RESULT 1

AR177880

LOCUS AR177880 4301 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 3 from patent US 6313276.

ACCESSION AR177880

VERSION AR177880.1 GI:17920235

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 4301)

AUTHORS Imura,H., Nakao,K. and Nakanishi,S.

TITLE Human endothelin receptor

JOURNAL Patent: US 6313276-A 3 06-NOV-2001;

FEATURES Location/Qualifiers

source 1. .4301

/organism="unknown"

BASE COUNT 1342 a 828 c 817 g 1314 t

ORIGIN

Query Match 100.0%; Score 4301; DB 6; Length 4301;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Db	1	GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC	60
Qy	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
Qy	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240

Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140

Db	1081	 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	 TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	 TAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Db	1801	 TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980

Db	1921	AATCAATGGGACTCTGATATAAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAAACAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAAACAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAATAGAAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820

Qy	2821	ACATGGTGTCTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	ACATGGTGTCTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	AGCTTTGTGCGTTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Db	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	GAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTCATTTCAGTGGCTT	3660
Db	3601	TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTCATTTCAGTGGCTT	3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720
 |||
 Db 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780
 |||
 Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840
 |||
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
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 Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
 |||
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
 |||
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
 |||
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140
 |||
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
 |||
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
 |||
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301

RESULT 2

E07650

LOCUS E07650 4301 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding endothelin receptor, ETB-receptor.

ACCESSION E07650

VERSION E07650.1 GI:2175785

KEYWORDS JP 1994157595-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4301)

Db	181	AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCTTGTGTTCTGCTGCTGGGGATCATCGGGAAGTCCACA	600
Db	541	TACATCAACACGGTTGTGTCTGCTTGTGTTCTGCTGCTGGGGATCATCGGGAAGTCCACA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080

Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920

Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACCTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTTGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTTGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCAGCATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCAGCATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Db	2341	CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Db	2701	GCTATAGTTAAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820

Db	2761	 TAAAGCTTATTACTAATTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTGAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTGAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Db	3001	 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Db	3241	 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Db	3541	 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600
Qy	3601	TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAAATTGCATTTCAGTGGCTT	3660

Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660

Qy 3661 TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720
 |||

Db 3661 TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780
 |||

Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840
 |||

Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
 |||

Db 3841 CAGCTCAAAGATTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
 |||

Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020
 |||

Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
 |||

Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140
 |||

Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
 |||

Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
 |||

Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAA 4301
 |||

Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAA 4301

RESULT 3

HUMETR

LOCUS HUMETR 4286 bp mRNA linear PRI 18-DEC-2002

DEFINITION Homo sapiens ETR mRNA for endothelin receptor, complete cds.

ACCESSION D90402

VERSION D90402.1 GI:219651

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTTGGAGTCTGGACATCTGA	180
Qy	181	AACTTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Db	181	AACTTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG	240
Qy	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG	300
Db	241	CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG	300
Qy	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Db	301	TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA	360
Qy	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Db	361	ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT	420
Qy	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Db	421	CTGGCGCGGTCTGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG	480
Qy	481	CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Db	481	CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA	540
Qy	541	TACATCAACACGGTTGTGTCTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAATCCACA	600
Db	541	TACATCAACACGGTTGTGTCTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAATCCACA	600
Qy	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAAATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTAG	1020

Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACCTGAATTCCCTGCATT	1380
Db	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACCTGAATTCCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA	1440
Qy	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Db	1441	TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA	1500
Qy	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCAGTAATAAATACAGCTCA	1560
Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCAGTAATAAATACAGCTCA	1560
Qy	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Db	1561	TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA	1620
Qy	1621	AACAAAATGAAACATTTGCCAAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Db	1621	AACAAAATGAAACATTTGCCAAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
Qy	1681	TAAAAATATTAAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Db	1681	TAAAAATATTAAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740
Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860
Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT	1860

Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTTAAATTTTAAATCCTTTAAAAACAACCTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTTAAATTTTAAATCCTTTAAAAACAACCTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Db	2161	TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
Qy	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Db	2221	CAACATGTCAAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
Qy	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Db	2281	TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
Qy	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Db	2341	CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA	2400
Qy	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Db	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
Qy	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
Qy	2581	GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Db	2581	GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGAGTGTCCACATGACAAAGGG	2640
Qy	2641	GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Db	2641	GCAGGTAGCACCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT	2700
Qy	2701	GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760

Db	2701	 GCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG	2760
Qy	2761	TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Db	2761	 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG	2820
Qy	2821	ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Db	2821	 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT	2880
Qy	2881	AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Db	2881	 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT	2940
Qy	2941	GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Db	2941	 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG	3000
Qy	3001	GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Db	3001	 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCAATGCCT	3060
Qy	3061	CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Db	3061	 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA	3120
Qy	3121	GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Db	3121	 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA	3180
Qy	3181	ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Db	3181	 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG	3240
Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Db	3241	 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
Qy	3301	GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Db	3301	 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC	3360
Qy	3361	ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Db	3361	 ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT	3420
Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Db	3421	 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
Qy	3481	TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Db	3481	 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA	3540
Qy	3541	TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT	3600

Db	481	 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA	540
Qy	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGA	600
Db	541	TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGA	600
Qy	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Db	601	CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC	660
Qy	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Db	661	AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG	720
Qy	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
Qy	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Db	781	AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA	840
Qy	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAA	900
Db	841	GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAA	900
Qy	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
Qy	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
Qy	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
Qy	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Qy	1201	GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Db	1201	GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
Qy	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380

Db	1321	AGCTTTCTGTTGGTATTGGACTATATTTGGTATCAACATGGCTTCACTGAATTCCCTGCATT	1380
Qy	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTA	1440
Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTA	1440
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Qy	1621	AACAAAATGAAACATTTTGCCAAAACAAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
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Db	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA	1920
Qy	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
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Qy	3241	TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA	3300
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Qy	3421	CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA	3480
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Db	3721	TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT	3780
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Db	3781	TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA	3840
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Db	3841	CAGCTCAAAAGATTTATAAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT	3900
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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 5

AX587707

LOCUS AX587707 4286 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 177 from Patent WO0246467.

ACCESSION AX587707

VERSION AX587707.1 GI:28212378

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and Fert,V.

TITLE Gene expression profiling of primary breast carcinomas using arrays of candidate genes

JOURNAL Patent: WO 0246467-A 177 13-JUN-2002; Ipsogen (FR)

FEATURES Location/Qualifiers

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/db_xref="taxon:32630"
/note="primer"

misc_feature 1. .4286
/note="endothelin receptor type b (EDNRB) gene."

BASE COUNT 1327 a 829 c 816 g 1314 t

ORIGIN

Query Match 99.6%; Score 4284.4; DB 6; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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      |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
      |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
      |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

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      |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
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Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

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Db    781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840
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Qy	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Db	1741	TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT	1800
Qy	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACTTCCAGGATATTCACACAACACT	1860
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Qy	1861	TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT	1920
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Db	1921	AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG	1980
Qy	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACACTTTTCAATTAATAT	2040
Db	1981	AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Qy	2161	TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC	2220
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Db	2581		GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
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Qy	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
Db	4141	ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA	4200
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QY 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

S57283

LOCUS S57283 4286 bp mRNA linear PRI 18-MAR-2002

DEFINITION Homo sapiens endothelin ET-B receptor mRNA, complete cds.

ACCESSION S57283

VERSION S57283.1 GI:298321

KEYWORDS

SOURCE	Homo sapiens (human)
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4286)

AUTHORS Arai, H., Nakao, K., Hosoda, K., Ogawa, Y., Nakagawa, O., Komatsu, Y. and Imura, H.

TITLE Molecular cloning of human endothelin receptors and their expression in vascular endothelial cells and smooth muscle cells

JOURNAL Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)

MEDLINE 93180293

PUBMED 1291713

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 128424] from the original journal article. This sequence comes from Fig. 5.

FEATURES	Location/Qualifiers
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1. 4286

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CDS

238.1566

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0:

Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	61	AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG	120
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Db	121	AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA	180
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Db	721	CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG	780
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Db	901	ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT	960
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Db	961	ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG	1020
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Db	1021	AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT	1080
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Db	1081	TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG	1140
Qy	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
Db	1141	AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG	1200
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Db	1201	GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC	1260
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Db	1261	AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG	1320
Qy	1321	AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT	1380
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Db	1381	AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA	1440
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Db	1501	AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA	1560
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Qy	1621	AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT	1680
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Db	1681	TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT	1740

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Db	1801	TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACT	1860
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Db	1981	AAGCTTAAATTACTCAATTTTAAAAATTTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT	2040
Qy	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Db	2041	TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT	2100
Qy	2101	TTTTTCGGACACTGGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
Db	2101	TTTTTCGGACACTGGAAACATTTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT	2160
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Qy	2221	CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA	2280
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Db	2281	TATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA	2340
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Db	2341	CAAAGAGAAATAGAAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA	2400
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Db	2401	CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTT	2460
Qy	2461	TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA	2520
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Db	2521	CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT	2580
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Db	2581	 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG	2640
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Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
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Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 7

D13162S7

LOCUS D13162S7 2972 bp DNA linear PRI 12-OCT-2002

DEFINITION Homo sapiens hET-BR gene for endothelin-B receptor, complete cds and exon 7.

ACCESSION D13168

VERSION D13168.1 GI:285924

KEYWORDS .

SEGMENT 7 of 7

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2972)

AUTHORS Arai,H., Nakao,K., Takaya,K., Hosoda,K., Ogawa,Y., Nakanishi,S. and Imura,H.

TITLE The human endothelin-B receptor gene. Structural organization and chromosomal assignment

JOURNAL J. Biol. Chem. 268 (5), 3463-3470 (1993)

MEDLINE 93155196

PUBMED 8429023

REFERENCE 2 (bases 1 to 2972)

AUTHORS Arai,H.

TITLE Direct Submission

JOURNAL Submitted (02-SEP-1992) Hiroshi Arai, Kyoto University School of Medicine, Second Division, Department of Medicine; 54 Shogoin, Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan (Tel:81-75-751-3170, Fax:81-75-771-9452)

FEATURES Location/Qualifiers

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D13167.1:11. .119,11. .2865)

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ORIGIN

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Matches 2857; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      129 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACC 188

Qy      1610 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCA 1669
          |||
Db      189 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCA 248

Qy      1670 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT 1729
          |||
Db      249 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT 308

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGA 1789
          |||
Db      309 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGA 368

Qy      1790 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849
          |||
Db      369 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 428

Qy      1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909
          |||
Db      429 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 488

Qy      1910 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGA 1969
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Db      489 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGA 548

Qy      1970 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT 2029
          |||
Db      549 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT 608

Qy      2030 TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT 2089
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Db      609 TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT 668

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Qy	2090	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG	2149
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Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTTCTG	2209
Db	729	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTTCTG	788
Qy	2210	CAATATGTAACCAACATGTGCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGC	2269
Db	789	CAATATGTAACCAACATGTGCACAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGC	848
Qy	2270	TGAATTTAAATATAAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG	2329
Db	849	TGAATTTAAATATAAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG	908
Qy	2330	ATCAAACCTCACAAAGAGAAAATAGAAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAA	2389
Db	909	ATCAAACCTCACAAAGAGAAAATAGAAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAA	968
Qy	2390	TCTGTCAATTCACATACCCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA	2449
Db	969	TCTGTCAATTCACATACCCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA	1028
Qy	2450	ATCTTCTTTTTTTCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTT	2509
Db	1029	ATCTTCTTTTTTTCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTGCATCTGTAAATACTT	1088
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	1089	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	1148
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCAC	2629
Db	1149	GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCAC	1208
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGC	2689
Db	1209	ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAAATGGTTTCTAGC	1268
Qy	2690	ATATGTATAAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA	2749
Db	1269	ATATGTATAAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA	1328
Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTTGTTATTATTTTTGTAAATAGCCAAATAGAA	2809
Db	1329	ACAGCTACCTGTAAAGCTTATTACTAATTTTTTGTTATTATTTTTGTAAATAGCCAAATAGAA	1388
Qy	2810	AAGTTTGCCTTGACATGGTGCCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGT	2869
Db	1389	AAGTTTGCCTTGACATGGTGCCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTTGAGACCGT	1448
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	2929
Db	1449	AAGAACCTCTTAGCTTTGTGCGTTCCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	1508

Qy	2930	TAGGATAGCTTGGGATGAGATGTTGTGTGAAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG	2989
Db	1509	TAGGATAGCTTGGGATGAGATGTTGTGTGAAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG	1568
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTT	3049
Db	1569	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTT	1628
Qy	3050	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	3109
Db	1629	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	1688
Qy	3110	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
Db	1689	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	1748
Qy	3170	AATATGCCCAAATTTTACTTTTGTTTTCTTTTAATAGGCTGGGGCCACATGTTGGAAATA	3229
Db	1749	AATATGCCCAAATTTTACTTTTGTTTTCTTTTAATAGGCTGGGGCCACATGTTGGAAATA	1808
Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	3289
Db	1809	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	1868
Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
Db	1869	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	1928
Qy	3350	ATAAATCACCCACAAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
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Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
Db	1989	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	2048
Qy	3470	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	3529
Db	2049	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	2108
Qy	3530	GAATTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	2109	GAATTTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC	2168
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	3649
Db	2169	TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA	2228
Qy	3650	TTCAGTGGCTTTTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	3709
Db	2229	TTCAGTGGCTTTTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA	2288
Qy	3710	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	3769
Db	2289	ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT	2348
Qy	3770	TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	3829

Db	2349		TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA	2408
Qy	3830		CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	3889
Db	2409		CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT	2468
Qy	3890		CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	3949
Db	2469		CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC	2528
Qy	3950		AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	4009
Db	2529		AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA	2588
Qy	4010		TATAACAATGTAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	4069
Db	2589		TATAACAATGTAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA	2648
Qy	4070		GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACA	4129
Db	2649		GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACA	2708
Qy	4130		CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAA	4189
Db	2709		CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAA	2768
Qy	4190		TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTAT	4249
Db	2769		TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTAT	2828
Qy	4250		GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	4286
Db	2829		GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG	2865

RESULT 8

AL139002/c

LOCUS AL139002 183337 bp DNA linear PRI 28-JAN-2001

DEFINITION Human DNA sequence from clone RP11-318G21 on chromosome 13q22.2-31.1, complete sequence.

ACCESSION AL139002

VERSION AL139002.18 GI:12597038

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 183337)

AUTHORS Wall,M.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Jan 29, 2001 this sequence version replaced gi:12584355. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr13>

RP11-318G21 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-318G21 The true left end of clone RP11-267I18 is at 125528 in this sequence.

FEATURES	Location/Qualifiers
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repeat_region	1216. .1308 /note="HAL1 repeat: matches 1475. .1563 of consensus"
repeat_region	1309. .1597 /note="AluJb repeat: matches 1. .297 of consensus"
repeat_region	1598. .2044 /note="HAL1 repeat: matches 1003. .1475 of consensus"
repeat_region	2148. .2276 /note="L2 repeat: matches 2620. .2749 of consensus"
repeat_region	2330. .2378 /note="L2 repeat: matches 2442. .2492 of consensus"
repeat_region	3915. .4224 /note="AluY repeat: matches 1. .306 of consensus"
repeat_region	4617. .4750 /note="67 copies 2 mer cc 61% conserved"
repeat_region	4648. .4727 /note="20 copies 4 mer cctt 78% conserved"
repeat_region	4729. .4784 /note="14 copies 4 mer tcct 78% conserved"
repeat_region	5431. .5736 /note="AluSx repeat: matches 1. .305 of consensus"
repeat_region	11990. .12273 /note="AluSx repeat: matches 9. .292 of consensus"

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repeat_region	13390. .13519
	/note="L2 repeat: matches 2410. .2548 of consensus"
repeat_region	14630. .14978
	/note="THE1B repeat: matches 1. .360 of consensus"
repeat_region	15092. .15580
	/note="L1MB1 repeat: matches 5656. .6116 of consensus"
repeat_region	15581. .16095
	/note="L1PA7 repeat: matches 5629. .6143 of consensus"
repeat_region	16096. .16549
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repeat_region	16731. .16777
	/note="MIR repeat: matches 35. .78 of consensus"
repeat_region	16778. .17137
	/note="THE1C repeat: matches 1. .371 of consensus"
repeat_region	17138. .17273
	/note="MIR repeat: matches 78. .226 of consensus"
repeat_region	17374. .17484
	/note="MIR repeat: matches 26. .158 of consensus"
repeat_region	17485. .17777
	/note="AluSc repeat: matches 1. .290 of consensus"
repeat_region	17778. .17815
	/note="MIR repeat: matches 158. .191 of consensus"
repeat_region	18981. .19048
	/note="34 copies 2 mer tt 66% conserved"
repeat_region	19447. .19589
	/note="MIR repeat: matches 131. .262 of consensus"
repeat_region	19843. .20162
	/note="MER33 repeat: matches 1. .324 of consensus"
repeat_region	20866. .21198
	/note="MER44A repeat: matches 3. .333 of consensus"
repeat_region	21742. .21878
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repeat_region	22214. .22310
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repeat_region	22321. .22418
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repeat_region	22419. .22730
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repeat_region	22731. .23714
	/note="L1MB8 repeat: matches 5130. .6078 of consensus"
repeat_region	23715. .24008
	/note="AluSg repeat: matches 1. .294 of consensus"
repeat_region	24009. .24264
	/note="L1MB8 repeat: matches 4884. .5130 of consensus"
repeat_region	24265. .24569
	/note="AluY repeat: matches 1. .305 of consensus"
repeat_region	24570. .25577
	/note="L1MB8 repeat: matches 3786. .4884 of consensus"
repeat_region	25582. .25635
	/note="27 copies 2 mer tt 70% conserved"
repeat_region	26221. .26571
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repeat_region	/note="AluY repeat: matches 1. .311 of consensus" 27067. .27134
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repeat_region	/note="MER39 repeat: matches 13. .381 of consensus" 29282. .29517
repeat_region	/note="MER39b repeat: matches 327. .579 of consensus" 30210. .30526
repeat_region	/note="AluJo repeat: matches 1. .303 of consensus" 31423. .31572
repeat_region	/note="L1PA13 repeat: matches 6005. .6155 of consensus" 31587. .31624
repeat_region	/note="19 copies 2 mer tt 86% conserved" 32103. .32181
repeat_region	/note="ORSL repeat: matches 390. .467 of consensus" 33878. .34312
repeat_region	/note="MER57A repeat: matches 1. .433 of consensus" 36673. .36768
repeat_region	/note="LTR37A repeat: matches 81. .172 of consensus" 36769. .37066
repeat_region	/note="AluSq repeat: matches 1. .296 of consensus" 37067. .37300
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repeat_region	/note="L1M4 repeat: matches 1085. .1580 of consensus" 43703. .44007
repeat_region	/note="AluJb repeat: matches 1. .305 of consensus" 44019. .44180
repeat_region	/note="L1MD1 repeat: matches 6044. .6211 of consensus" 44183. .44485
repeat_region	/note="AluJo repeat: matches 1. .300 of consensus" 44486. .44611
repeat_region	/note="L1MD2 repeat: matches 5949. .6066 of consensus" 45256. .45430
repeat_region	/note="MER5B repeat: matches 1. .178 of consensus" 45588. .45669
repeat_region	/note="MER5A repeat: matches 109. .188 of consensus" 46919. .47084
repeat_region	/note="MIR repeat: matches 94. .260 of consensus" 47873. .47902
repeat_region	/note="15 copies 2 mer tg 90% conserved" 49906. .49933
repeat_region	/note="7 copies 4 mer tgtg 96% conserved" 50452. .50507
repeat_region	/note="LTR37A repeat: matches 128. .184 of consensus" 51786. .51829
repeat_region	/note="MER74A repeat: matches 271. .309 of consensus" 51830. .52172
repeat_region	/note="THE1B repeat: matches 1. .364 of consensus"

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Db	72170	AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG	72111
Qy	2150	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTG	2209
Db	72110	AGCAAGGCTGTTTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTG	72051
Qy	2210	CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	2269
Db	72050	CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC	71991
Qy	2270	TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG	2329
Db	71990	TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG	71931
Qy	2330	ATCAAACCTCACAAGAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA	2389
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Db	71870	TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA	71811
Qy	2450	ATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	2509
Db	71810	ATCTTCTTCTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT	71751
Qy	2510	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	2569
Db	71750	ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC	71691
Qy	2570	GATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	2629
Db	71690	GATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCAC	71631
Qy	2630	ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGC	2689
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Qy	2750	ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA	2809
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Qy	2810	AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	2869
Db	71450	AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT	71391
Qy	2870	AAGAACCTCTTAGCTTTGTGCGTTCCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT	2929
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Qy	2930	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	2989
Db	71330	TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG	71271
Qy	2990	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	3049
Db	71270	GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT	71211
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Db	71210	CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG	71151
Qy	3110	CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA	3169
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Qy	3170	AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA	3229
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Qy	3230	AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA	3289
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Qy	3290	CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT	3349
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Qy	3350	ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT	3409
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Qy	3410	ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA	3469
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Qy	3470	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	3529
Db	70790	CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT	70731
Qy	3530	GAATTTTTTACATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATC	3589
Db	70730	GAATTTTTTACATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTCTAATTATC	70671
Qy	3590	TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCA	3649
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Qy 4070 GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAATA 4129
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Qy 4130 CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189
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 Db 70011 GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG 69975

RESULT 9

AC144750/c

LOCUS AC144750 201093 bp DNA linear HTG 04-JUN-2003

DEFINITION Pan troglodytes clone CH251-517B22, WORKING DRAFT SEQUENCE, 3 ordered pieces.

ACCESSION AC144750

VERSION AC144750.2 GI:31376422

KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 201093)

AUTHORS Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,

Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.

TITLE NISC Comparative Sequencing Initiative
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 201093)
 AUTHORS Green,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2003) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 REFERENCE 3 (bases 1 to 201093)
 AUTHORS Green,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUN-2003) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 COMMENT On Jun 4, 2003 this sequence version replaced gi:30725907.
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc_zoo@nhgri.nih.gov
 ----- Project Information
 Center project name: esg
 Center clone name: 517B22

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 200649 bases at least Q40
 Consensus quality: 200775 bases at least Q30
 Consensus quality: 200836 bases at least Q20
 Insert size: 165000; agarose-fp
 Insert size: 200893; sum-of-contigs
 Quality coverage: 13.47x in Q20 bases; agarose-fp
 Quality coverage: 11.07x in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and

* the accession number will be preserved.
 * 1 107546: contig of 107546 bp in length
 * 107547 107646: gap of unknown length
 * 107647 153000: contig of 45354 bp in length
 * 153001 153100: gap of unknown length
 * 153101 201093: contig of 47993 bp in length.

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 misc_feature 83861. .201093
 /note="clone overlaps with GenBank Accession Number
 AC144499 clone RP43-108D19 (center project name esf)"
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 /note="assembly_fragment
 clone_end:SP6
 vector_side:right"

BASE COUNT 61806 a 36616 c 38060 g 64411 t 200 others
 ORIGIN

Query Match 64.9%; Score 2792.4; DB 2; Length 201093;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 2838; Conservative 0; Mismatches 16; Indels 6; Gaps 3;

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 Db 69717 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 69658
 Qy 1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
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 Db 69657 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 69598
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 Db 69597 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATCTCACTTTCTTTATATTGGACC 69538
 Qy 1610 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAAACAAAACAAAAAACTATGTATTTGCA 1669
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 Db 69537 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAAACAAAACAAAAAACTATGTATTTGCA 69478
 Qy 1670 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT 1729
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Qy	1790	AAGCACTTAATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	1849
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Db	68579	TACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTC	68520
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Db	68519	 CACATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCT	68460
Qy	2687	AGCATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACAT	2746
Db	68459	 AGCATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACAT	68400
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Qy	2807	GAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGAC	2866
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Qy	2867	CGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTG	2926
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Db	67979	 TAAATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAA	67920
Qy	3227	ATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACC	3286
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Qy	4067	ATAGTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACA	4126
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Qy	4187	AAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTAT	4246
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LOCUS G06417 2720 bp DNA linear STS 19-OCT-1995
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 ACCESSION G06417
 VERSION G06417.1 GI:859662
 KEYWORDS STS; STS sequence; primer; sequence tagged site.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2720)
 AUTHORS Hudson,T.
 TITLE Whitehead Institute/MIT Center for Genome Research; Physically
 Mapped ESTs
 JOURNAL Unpublished (1995)
 COMMENT
 Contact: Thomas Hudson
 Whitehead Institute/MIT Center for Genome Research
 Whitehead Institute for Biomedical Research
 9 Cambridge Center, Cambridge MA 02142 USA
 Tel: 617 252 1900
 Fax: 617 252 1902
 Email: thudson@genome.wi.mit.edu

 Primer A: ATGGAGAGATGCCAGTGACC
 Primer B: TAGGCAGGAACGCACAAAG
 STS size: 331
 PCR Profile:
 Presoak:
 Denaturation:
 Annealing: 56 degrees C
 Polymerization:
 PCR Cycles: 35
 Thermal Cycler:
 Protocol:
 Template: 10 ng
 Primer: each 5 pM
 dNTPs: each 4 nM
 Taq Polymerase: 0.025 units/ul
 Total Vol: 20 ul

 Buffer:
 MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCL: 10 mM
 pH: 9.3

 Prepared with primer pairs derived from D90402 -- Unigene.
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 primer_bind complement(1317. .1335)

BASE COUNT 894 a 438 c 408 g 870 t 110 others
ORIGIN

Query Match 60.7%; Score 2610; DB 11; Length 2720;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 2610; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Qy      1927 TGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATGAAGCTT 1986
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Qy      2287 ACTTTTAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCACAAAGA 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||
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Db	721	ACTTTTAAAAAGAAAATTATTACATCCTTTACATTCACTTAAGATCAAACCTCACAAAGA	780
Qy	2347	GAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCACATAACC	2406
Db	781	GAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCAATTCACATAACC	840
Qy	2407	CTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTTTCACTA	2466
Db	841	CTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTTTCACTA	900
Qy	2467	TCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACACTGCAT	2526
Db	901	TCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACACTGCAT	960
Qy	2527	GTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGT	2586
Db	961	GTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGT	1020
Qy	2587	GACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGT	2646
Db	1021	GACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGT	1080
Qy	2647	AGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAATGCTATA	2706
Db	1081	AGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAATGCTATA	1140
Qy	2707	GTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTGTAAAGC	2766
Db	1141	GTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTGTAAAGC	1200
Qy	2767	TTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGG	2826
Db	1201	TTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGG	1260
Qy	2827	TGCTTTTCTTTCATCTAGAGGCAAAAC TGCTTTT TGAGACCGTAAGAACCTCTTAGCTTT	2886
Db	1261	TGCTTTTCTTTCATCTAGAGGCAAAAC TGCTTTT TGAGACCGTAAGAACCTCTTAGCTTT	1320
Qy	2887	GTGCGTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTTGGGATG	2946
Db	1321	GTGCGTTCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTTGGGATG	1380
Qy	2947	AGATGTGTGTGAAAGTATGTACAAGAGAAAA CGGAAGAGAGAGGAAATGAGGTGGGGTTG	3006
Db	1381	AGATGTGTGTGAAAGTATGTACAAGAGAAAA CGGAAGAGAGAGGAAATGAGGTGGGGTTG	1440
Qy	3007	GAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTCGCTCAGTCA	3066
Db	1441	GAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTCGCTCAGTCA	1500
Qy	3067	ATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA	3126
Db	1501	ATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA	1560
Qy	3127	CTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAAATTTTT	3186
Db	1561	CTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAAATTTTT	1620

Qy	3187	ACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT	3246
Db	1621	ACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT	1680
Qy	3247	TCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCAGAAAGA	3306
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Qy	3307	AAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCCACAAAC	3366
Db	1741	AAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCCACAAAC	1800
Qy	3367	TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT	3426
Db	1801	TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT	1860
Qy	3427	AGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTTCAGTTTATTAATATATT	3486
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Qy	3547	TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC	3606
Db	1981	TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC	2040
Qy	3607	TACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTTTTTAAA	3666
Db	2041	TACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTTTTTNNN	2100
Qy	3667	AAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT	3726
Db	2101	NNNNNTGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT	2160
Qy	3727	ACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGTTTCCTA	3786
Db	2161	ACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGTTTCCTA	2220
Qy	3787	GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC	3846
Db	2221	GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC	2280
Qy	3847	AAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT	3906
Db	2281	AAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT	2340
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Db	2341	GTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACAGTTTAT	2400
Qy	3967	AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAAA	4026
Db	2401	AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAAA	2460

Qy 4027 TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTTATT 4086
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 Db 2461 TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTTATT 2520

Qy 4087 ATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTCACTGTA 4146
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 Db 2581 CAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGACAAGTG 2640

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RESULT 11

AC130785/c

LOCUS AC130785 169751 bp DNA linear HTG 29-AUG-2002

DEFINITION Papio anubis clone RP41-325P5, WORKING DRAFT SEQUENCE.

ACCESSION AC130785

VERSION AC130785.1 GI:22218455

KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.

SOURCE Papio anubis (olive baboon)

ORGANISM Papio anubis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 Cercopithecinae; Papio.

REFERENCE 1 (bases 1 to 169751)

AUTHORS Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
 Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
 Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,
 Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
 Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
 McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
 Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schueler,M.G., Sison,C.,
 Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
 Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169751)

AUTHORS Green,E.D.

TITLE Direct Submission

JOURNAL Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA

REFERENCE 3 (bases 1 to 169751)

AUTHORS Green,E.D.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2002) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA

COMMENT ----- Genome Center

Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nhgri.nih.gov

----- Project Information

Center project name: deh
Center clone name: 325P05

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 169735 bases at least Q40
Consensus quality: 169747 bases at least Q30
Consensus quality: 169749 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 169751; sum-of-contigs
Quality coverage: 10.99x in Q20 bases; agarose-fp
Quality coverage: 8.94x in Q20 bases; sum-of-contigs

- * NOTE: This is a 'working draft' sequence. It currently
- * consists of 1 contigs. Gaps between the contigs
- * are represented as runs of N. The order of the pieces
- * is believed to be correct as given, however the sizes
- * of the gaps between them are based on estimates that have
- * provided by the submitter.
- * This sequence will be replaced
- * by the finished sequence as soon as it is available and
- * the accession number will be preserved.
- * 1 169751: contig of 169751 bp in length.

FEATURES

source

Location/Qualifiers
1. .169751
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/mol_type="genomic DNA"
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/clone_lib="RP41"

misc_feature

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/note="assembly_fragment
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vector_side:left
clone_end:Sp6
vector_side:right"

misc_feature

1. .63149

/note="clone overlaps with GenBank Accession Number
AC129069 clone RP41-240D13 (center project name deg)"

BASE COUNT 51109 a 31316 c 31981 g 55345 t
ORIGIN

Query Match 59.3%; Score 2550; DB 2; Length 169751;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2717; Conservative 0; Mismatches 130; Indels 19; Gaps 7;

Qy	1430	AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC	1489
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Qy	1490	AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA	1549
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Qy	1550	AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACC	1609
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Qy	1610	GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA	1669
Db	29038	GAAGTCATTAAAAACAAAATGAAACATTTGTCAAAAACAAAACAAAAAACTATGTATTTGCA	28979
Qy	1670	CAGCACACTATTAAAAATATTAAGTGTAAATATTTTAACTCACAGCTACATATGACATT	1729
Db	28978	CAGCACACTATTAAAAATATTAAGTGTAAATATTTTAACTCATAGCTACATATGACATT	28919
Qy	1730	TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA	1789
Db	28918	TTATGAGCTGTTTACAGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCATTGTGA	28859
Qy	1790	AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT	1849
Db	28858	AAGCACTTACTTTTTTATGGTTAGCACTTCAACATAGCTCTTAATAACTCCAGGATATT	28799
Qy	1850	CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAG	1909
Db	28798	CACACAACCCTTAGGCTTAAAAATGAGCTCACTCGGAATTTCTATT-----TAAGAG	28747
Qy	1910	ATTTATTTTTTAAATCAATGGGACTCTGATATAAGGAAGAATAAGTCACTGTAAACAGA	1969
Db	28746	ATTTATTTTTTAAATCAATGTGAATCTGATACAAAGGAAGAGTAAGTCACTGTAAACAGA	28687
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACTTT	2029
Db	28686	ACTTTTAAATGAAGCTTAAATTACCCAATTTGAAATTTTAAAAATCCTTTAAAGAACTTT	28627
Qy	2030	TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT	2088
Db	28626	TTAATTAATATTTTCACTGCTGATCAGACTGTAATTAGATGCAAATGAGAGAGTAGTT	28567
Qy	2089	TAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA	2148
Db	28566	TAGTTGCTGTATTTTTTGGACACTAGAAACATTTAAATGATCAGGAGGGAGTAACTGAAA	28507

Qy	2149	GAGCAAGGCTGTTTTTTTGAAAATCATTACA---CTTTCACTAGAAGCCCAACCTCAGCAT	2205
Db	28506	GAACAAGGCTGTTTTTTGAAAATCATTACACTCCTTTCACTAGAAGCCCAACCTCAGCAT	28447
Qy	2206	TCTGCAATATGTAACCAACATGTCAAAACAAGCAGCATGTAAACAGACTGGCACATGTGC	2265
Db	28446	TCTGCAATATGTAACCAACATGTTACAAACAAGCAGCATGTAAACAACTGGCACATGTGT	28387
Qy	2266	CAGCTGAATTTAAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCACT	2325
Db	28386	CAGCCAAATCTAAAAATATAATACTTTTAAAAAGAAAATTATTACACCCTTTACATTCACT	28327
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Db	28326	TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTGCCCAAAAGACTTCTT	28267
Qy	2386	TGAATCTGTCATTACATACCCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT	2445
Db	28266	TGAATCTGCCATTACACAGCCTGTGAAGAAAATACTATCTACAATTTTTTTCAGGATTAT	28207
Qy	2446	TAAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT	2505
Db	28206	TAAAAATCTTCTTCTTTCACTATTGTAGCTTAAACTCTGTTTGGTTTTGTCATCCGTAAAT	28147
Qy	2506	ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT	2565
Db	28146	ACTTAGCTACATACACTGCATGTAGACGATTAAACGAGGGCGGGCCCTGTGTTTCATAGTT	28087
Qy	2566	TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGT	2625
Db	28086	TTACAATGGAGAGATGCCAGTGACCTCATAATAGAGACTGTGAACTGCCTGGTGCAGTGT	28027
Qy	2626	CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTC	2685
Db	28026	CCACATGACAAGGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTAGTTAAAATGGTTTC	27967
Qy	2686	TAGCATATGTATAATGCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACA	2745
Db	27966	TAGCATATGTATAATGCTGTAGTTAAAAACTGTTTTTGCAAAATCATACAGATTAGTACA	27907
Qy	2746	TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAAT	2805
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Qy	2806	AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCCAAACTGCTTTTTTGAGA	2865
Db	27846	AGAAAAGTGTGCTTGACGTGGTGCTTTTCTTTCACTTAGAGGCCAAACTGCTTTTTTGAGA	27787
Qy	2866	CCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGT	2925
Db	27786	CTGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTAAATCTTCTAAGCAAAGT	27727
Qy	2926	GCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG	2985
Db	27726	GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG	27667
Qy	2986	AGAGGAAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAA	3045

Db	27666	 AGAGGAAATGAGGTGGGGTGAGAGGAACTCATGGGGACAGATTCCCATTCTTAGCCTAA	27607
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Db	27606	 CGTTCGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACAC	27547
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Db	27546	 AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC	27487
Qy	3166	TTAAAATATGCCCAAATTTTTACTTTTGTCTTTTAAATAGGCTGGGCCACATGTTGGA	3225
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Qy	3226	AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAAC	3285
Db	27426	 AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAAC	27367
Qy	3286	CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT	3345
Db	27366	 CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT	27307
Qy	3346	ATTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC	3405
Db	27306	 ATTTATAAATCACCCACAACTTGTTTTTTAATTTTCATCCCAATCATTTTTTTCAGAGGCC	27247
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Db	27246	 TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAATTTTGAATCACTAATATT	27187
Qy	3466	TTCACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCAT	3524
Db	27186	 TTCACAGTTTATTAATATATTTTTATTTCTATTTAAATTTTAGATTATTTTTATTACCAT	27127
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Db	27126	 GTACTGAATTTTTATATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTGTAA	27067
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Qy	3645	TTGCATTTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT	3704
Db	27006	 TTGCATTTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT	26948
Qy	3705	AAGAAACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTT	3764
Db	26947	 AAGAAACAATAATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATTATT	26888
Qy	3765	CAACTTCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT	3824
Db	26887	 TAACCTTCAAAACATGTTTCCTAGTATTAAGAACTTTAATATAGCAACAGACAAAATTATT	26828
Qy	3825	GTTAACATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT	3884

Db 26827 GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACTATTTTCTCCCTT 26768
 Qy 3885 ATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATA 3944
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 Db 26767 ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA 26708
 Qy 3945 TGGCCAAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAG 4004
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 Db 26647 TGTAATATAACAATGTAAAAAATTATATACCTGGGGGGATTTTTTGGTTGCTTAAAGTGG 26588
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RESULT 12

AC129069/c

LOCUS AC129069 185870 bp DNA linear HTG 19-SEP-2002
 DEFINITION Papio anubis clone RP41-240D13, WORKING DRAFT SEQUENCE.
 ACCESSION AC129069
 VERSION AC129069.2 GI:23196382
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
 SOURCE Papio anubis (olive baboon)
 ORGANISM Papio anubis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 Cercopithecinae; Papio.
 REFERENCE 1 (bases 1 to 185870)
 AUTHORS Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
 Cariaga,K., Coleman,B., Dietrich,N.L., Granite,S., Guan,X.,
 Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R.,
 Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L.,
 Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,
 Mastrian,S.D., McCloskey,J.C., McDowell,J., Paguirigan,C.,
 Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N.,
 Schueler,M.G., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J.,
 Touchman,J.W., Vogt,J.L., Walker,M., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.
 TITLE NISC Comparative Sequencing Initiative
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 185870)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 185870)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT On Sep 19, 2002 this sequence version replaced gi:21955004.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: deg
Center clone name: 240D13

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 184076 bases at least Q40
Consensus quality: 185363 bases at least Q30
Consensus quality: 185733 bases at least Q20
Insert size: 152000; agarose-fp
Insert size: 185870; sum-of-contigs
Quality coverage: 7.20x in Q20 bases; agarose-fp
Quality coverage: 5.89x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 185870: contig of 185870 bp in length.

FEATURES
source Location/Qualifiers
1. 185870
/organism="Papio anubis"

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misc_feature 1. .185870
              /note="assembly_fragment
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              vector_side:left
              missing approximately 55 bases, including Sp6 clone end,
              on 3' end of insert"
misc_feature 121812. .185870
              /note="clone overlaps with GenBank Accession Number
              AC130785 clone RP41-325P5 (center project name deh)"
BASE COUNT   55300 a  34781 c  35402 g  60387 t
ORIGIN

Query Match          59.3%;  Score 2550;  DB 2;  Length 185870;
Best Local Similarity 94.8%;  Pred. No. 0;
Matches 2717;  Conservative 0;  Mismatches 130;  Indels 19;  Gaps 7;

Qy      1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
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Db      151685 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC
151626

Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
          |||
Db      151625 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA
151566

Qy      1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACC 1609
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Db      151565 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACC
151506

Qy      1610 GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 1669
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Db      151505 GAAGTCATTAAAAACAAAATGAAACATTTGTCAAAAACAAAACAAAAAACTATGTATTTGCA
151446

Qy      1670 CAGCACACTATTAAAATATTAAGTGTAATTATTTTAACTACTCACAGCTACATATGACATT 1729
          |||
Db      151445 CAGCACACTATTAAAATATTAAGTGTAATTATTTTAACTCATAGCTACATATGACATT
151386

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGA 1789
          |||
Db      151385 TTATGAGCTGTTTACAGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCATTGTGA
151326

Qy      1790 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849
          |||
Db      151325 AAGCACTTACTTTTTTATGGTTAGCACTTCAACATAGCTCTTAATAAATCCAGGATATT
151266

Qy      1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909
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Db	151265	CACACAACCCTTAGGCTTAAAAATGAGCTCACTCGGAATTTCTATT-----TAAGAG	
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Db	151213	ATTTATTTTTTAAATCAATGTGAATCTGATACAAAGGAAGAGTAAGTCACTGTAAACAGA	
151154			
Qy	1970	ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACTTT	2029
Db	151153	ACTTTTAAATGAAGCTTAAATTACCCAATTTGAAATTTTAAAAATCCTTTAAAGAACTTT	
151094			
Qy	2030	TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT	2088
Db	151093	TTAATTAATATTTTCACACTGCTGATCAGACTGTAATTAGATGCAAATGAGAGAGTAGTT	
151034			
Qy	2089	TAGTTGTTGCATTTTTTCGGACACTGGAACATTTAAATGATCAGGAGGGAGTAACAGAAA	2148
Db	151033	TAGTTGCTGTATTTTTTGGACACTAGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA	
150974			
Qy	2149	GAGCAAGGCTGTTTTTGAAAATCATTACA---CTTTCACTAGAAGCCCAAACCTCAGCAT	2205
Db	150973	GAACAAGGCTGTTTTTGAAAATCATTACACTCCTTTCACTAGAAGCCCAAACCTCAGCAT	
150914			
Qy	2206	TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC	2265
Db	150913	TCTGCAATATGTAACCAACATGTTACAAACAAGCAGCATGTAACAAACTGGCACATGTGT	
150854			
Qy	2266	CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCACT	2325
Db	150853	CAGCCAAATCTAAAATATAATACTTTTAAAAAGAAAATTATTACACCTTTACATTCACT	
150794			
Qy	2326	TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTT	2385
Db	150793	TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTGCCCCAAAGACTTCTT	
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Qy	2386	TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTAT	2445
Db	150733	TGAATCTGCCATTACACAGCCTGTGAAGAAAAATACTATCTACAAATTTTTTCAGGATTAT	
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Qy	2446	TAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAAT	2505
Db	150673	TAAAATCTTCTTCTTTCACTATTGTAGCTTAAACTCTGTTTGGTTTTGTCTATCCGTAAAT	
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Qy	2506	ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT	2565
Db	150613	ACTTAGCTACATACACTGCATGTAGACGATTAAACGAGGGCGGGCCCTGTGTTTCATAGTT	
150554			

Qy	2566	TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCACTGT	2625
Db	150553	TTACAAATGGAGAGATGCCAGTGACCTCATAATAGAGACTGTGAACTGCCCTGGTGCGATGT	
	150494		
Qy	2626	CCACATGACAAAGGGGCGAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTC	2685
Db	150493	CCACATGACAAAGGGGCGAGGTAGCACCCCTCTCTACCCATGCTGTAGTTAAATGGTTTC	
	150434		
Qy	2686	TAGCATATGTATAATGCTATAGTTAAAAATACTATTTTTCAAATCATAAGATTAGTACA	2745
Db	150433	TAGCATATGTATAATGCTATAGTTAAAAACTGTTTTGCAAATCATAAGATTAGTACA	
	150374		
Qy	2746	TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT	2805
Db	150373	TTTAATGGCTACCTGTAAAGCTTATTACTAGTTTTGTATTATTTTTGTAAATAGCCAAT	
	150314		
Qy	2806	AGAAAAAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGA	2865
Db	150313	AGAAAAAGTTTGCTTGACGTGGTGCTTTTCTTTCACTAGAGGCAAACTGCTTTTTGAGA	
	150254		
Qy	2866	CCGTAAGAACCCTCTTAGCTTTGTGCGTTCTGCTAATTTTTATATCTTCTAAGCAAAGT	2925
Db	150253	CTGTAAGAACCCTCTTAGCTTTGTGCGTTCTGCTAATTTTTAAATCTTCTAAGCAAAGT	
	150194		
Qy	2926	GCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG	2985
Db	150193	GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG	
	150134		
Qy	2986	AGAGGAAATGAGGTGGGGTTGGAGGAAACCATGGGGACAGATTCCCATTTCTAGCCTAA	3045
Db	150133	AGAGGAAATGAGGTGGGGTGAGAGGAAACTCATGGGGACAGATTCCCATTTCTAGCCTAA	
	150074		
Qy	3046	CGTTCGTCATTGCCTCGTCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACAC	3105
Db	150073	CGTTCGTCATTGCCTCGTCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACAC	
	150014		
Qy	3106	AGTGCAATGTTCTCAGAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC	3165
Db	150013	AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC	
	149954		
Qy	3166	TTAAAAATAGCCCAAATTTTTACTTTTGTCTTTTAAATAGGCTGGGCCACATGTTGGA	3225
Db	149953	TTAAAAATAGCCCAAATTTTTACTTTTTTTCTTTTAGTAACTGGGCCACATGTTGGA	
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Qy	3226	AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAAC	3285

Db	149833		AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAC	
	149834			
Qy	3286		CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT	3345
Db	149833		CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT	
	149774			
Qy	3346		ATTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC	3405
Db	149773		ATTTATAAATCACCCACAACTTGTTTTTAATTTTCATCCCAATCATTTTTTTCAGAGGCC	
	149714			
Qy	3406		TGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATT	3465
Db	149713		TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAATTTTGAATCACTAATATT	
	149654			
Qy	3466		TTCACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCAT	3524
Db	149653		TTCACAGTTTATTAATATATTTTTATTCTATTTAAATTTTAGATTATTTTTATTACCAT	
	149594			
Qy	3525		GTAAGTGAATTTTACATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTCTAA	3584
Db	149593		GTAAGTGAATTTTATATCCTGATACCTTTCTCTCCATGTCAGTATCATGTTCTGTAA	
	149534			
Qy	3585		TTATCTTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAA	3644
Db	149533		TTATCTTACCAATTTTGAAACTGCACACAAAAGCATACTTGCATTATTTATAATAAAA	
	149474			
Qy	3645		TTGCATTTCAGTGGCTTTTTAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT	3704
Db	149473		TTGCATTTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT	
	149415			
Qy	3705		AAGAAACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTT	3764
Db	149414		AAGAAACAATAATAATTTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATTATT	
	149355			
Qy	3765		CAACTTCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT	3824
Db	149354		TAAGTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT	
	149295			
Qy	3825		GTTAACATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT	3884
Db	149294		GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT	
	149235			
Qy	3885		ATTATCCACTGCTAATGTGGATGTATGTTCAACACCTTTTAGTATTGATAGCTTACATA	3944

Db 149234 ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA
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Qy 3945 TGGCCAAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAG 4004
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149115

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Db 149114 TGTAATATAACAATGTAAAAAATTATATACCTGGGGGGATTTTTTGGTTGCTTAAAGTGG
149055

Qy 4065 CTATAGTTACTGA-TTTTTTATTATGTAAGCAAAACCAATAAA----AATTTAAGTTTTT 4119
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Db 149054 CTATAGTCACTGATTTTTTTATTATGTAAGCAAAACCAATAAACTTTAGTTGTGTTTTT
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Qy 4120 TTAACAACTACCTTATTTTTCTACTGTACAGACACTAATTCATTAAATACTAATTGATTGT 4179
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Db 148994 TTAACAACTAGCTTATTTTTCTATTGTACAGGCACTAATTCATTAAATACTAATTGACTGT
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Qy 4180 TTAAAAGAAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAG 4239
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148875

Qy 4240 CAAGTATGAAGTTATTCAATTAAATGCCACATTTCTGGTCTCTGG 4285
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Db 148874 GAAGTATGAAGTTATTCAATTAAATGCCACATTTCTGGTCTCTGG 148829

RESULT 13

AR165435

LOCUS AR165435 1873 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 13 from patent US 6280931.

ACCESSION AR165435

VERSION AR165435.1 GI:16240327

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Sakamoto,A. and Hanaoka,F.

TITLE Method for specifically amplifying a dystroglycan,
.alpha.-sarcoglycan, or endothelin Breceptor cDNA of an extremely
small

JOURNAL Patent: US 6280931-A 13 28-AUG-2001;

FEATURES Location/Qualifiers

source 1. .1873

/organism="unknown"

BASE COUNT 490 a 434 c 438 g 511 t

ORIGIN

Query Match 39.3%; Score 1691.8; DB 6; Length 1873;

Best Local Similarity 99.6%; Pred. No. 6.1e-293;

Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAAGATTGGTGGCTGTTTCAGTTTC	1077
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Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCCTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCCTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
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Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGTC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGTC	1370
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Db	1371	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAGCAGTCGTGC	1497
Db	1431	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1677
Db	1611	TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAATAATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	TATTAATAATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1730
Qy	1738	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1797
Db	1731	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAAC	1857
Db	1791	AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTACACAAC	1850

Qy 1858 ACTTAGGCTTAAAAATGAGCTCA 1880
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 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

RESULT 14

E15242

LOCUS E15242 1873 bp DNA linear PAT 28-JUL-1999

DEFINITION Human mRNA for endothelin B receptor, complete cds.

ACCESSION E15242

VERSION E15242.1 GI:5709925

KEYWORDS JP 1998057064-A/13.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Sakamoto, E. and Hanaoka, F.

TITLE SPECIFIC AMPLIFICATION OF MINOR GENE PRODUCT

JOURNAL Patent: JP 1998057064-A 13 03-MAR-1998;

RIKAGAKU KENKYUSHO

COMMENT OS Homo sapiens (human)

PN JP 1998057064-A/13

PD 03-MAR-1998

PF 16-AUG-1996 JP 1996216506

PI SAKAMOTO EIJI, HANAOKA FUMIO

PC C12N15/09, C07H21/02, C07H21/04//C12Q1/68;

CC strandedness: Double;

CC topology: Linear;

FH Key Location/Qualifiers

FH

FT source 1. .1873

FT /organism='Homo sapiens'

FT /tissue_type='peripheral blood' FT CDS

231. .1559

FT /product='endothelin B receptor'.

FEATURES Location/Qualifiers

source 1. .1873

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 490 a 434 c 438 g 511 t

ORIGIN

Query Match 39.3%; Score 1691.8; DB 6; Length 1873;

Best Local Similarity 99.6%; Pred. No. 6.1e-293;

Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237

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Db 171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297

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Db 231 ATGCAGCCGCCTCCAAGTCTGTGCGGACCGGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 290

Qy 298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357

Db	291	 CTGTGCGGATCTGGGGAGAGGAGAGAGGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG	350
Qy	358	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	417
Db	351	 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC	410
Qy	418	AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	477
Db	411	 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	470
Qy	478	CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	537
Db	471	 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	530
Qy	538	AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTC	597
Db	531	 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	 ACACTTCTGAGAATTATCTACAAGAACAGTGCATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	777
Db	711	 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	957
Db	891	 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	 GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	 CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	 TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197

Db	1131	TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257
Db	1191	GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC	1437
Db	1371	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
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Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1677
Db	1611	TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1730
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Db	1731	TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1857
Db	1791	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC	1850
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Db	1851	ACTTAGGCTTAAAAATGAGCTCA	1873

RESULT 15

S44866

LOCUS	S44866	1872 bp	mRNA	linear	PRI 07-MAY-1993
DEFINITION	ETB endothelin receptor [human, mRNA, 1872 nt].				
ACCESSION	S44866				
VERSION	S44866.1 GI:233233				

Qy	358	CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCCAAGGGTTCCAACGCC	417
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Qy	418	AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT	477
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Qy	478	CCGCCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC	537
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Db	531	AAATACATCAACACGGTTGTGTCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCC	590
Qy	598	ACACTTCTGAGAATTATCTACAAGAACAAGTG CATGCGAAACGGTCCCAATATCTTGATC	657
Db	591	ACACTTCTGAGAATTATCTACAAGAACAAGTG CATGCGAAACGGTCCCAATATCTTGATC	650
Qy	658	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	717
Db	651	GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC	710
Qy	718	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	777
Db	711	AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA	770
Qy	778	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	837
Db	771	CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT	830
Qy	838	CGAGCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	897
Db	831	CGAGCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA	890
Qy	898	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTT	957
Db	891	GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTT	950
Qy	958	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1017
Db	951	GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT	1010
Qy	1018	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC	1077
Db	1011	CAGAAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC	1070
Qy	1078	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG	1137
Db	1071	TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG	1130
Qy	1138	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1197
Db	1131	TTGAGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA	1190
Qy	1198	GTGGCCAAAACCGTCTTTTGCCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1257

Db	1191	 GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC	1250
Qy	1258	CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1317
Db	1251	 CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT	1310
Qy	1318	TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1377
Db	1311	 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC	1370
Qy	1378	ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGC	1437
Db	1371	 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGC	1430
Qy	1438	TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1497
Db	1431	 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC	1490
Qy	1498	TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1557
Db	1491	 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC	1550
Qy	1558	TCATCTTGAAAGAAGAACTATTCACTGTATTTCACTTTCTTTATATTGGACCGAAGTCAT	1617
Db	1551	 TCATCTTGAAAGAAGAACTATTCACTGTATTTCACTTTCTTTATATTGGACCGAAGTCAT	1610
Qy	1618	TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1677
Db	1611	 TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC	1670
Qy	1678	TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1737
Db	1671	 TATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC	1730
Qy	1738	TGTTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1797
Db	1731	 TGTTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT	1790
Qy	1798	AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAAC	1857
Db	1791	 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAAC	1850
Qy	1858	ACTTAGGCTTAAAAATGAGCTC	1879
Db	1851	 ACTTAGGCTTAAAAATGAGCTC	1872

Search completed: December 12, 2003, 19:39:19
 Job time : 15106.3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2003, 09:17:01 ; Search time 7748.55 Seconds
(without alignments)
13490.718 Million cell updates/sec

Title: US-09-931-157-2
Perfect score: 4301
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	1372.2	31.9	3878	11	AK083415	AK083415 Mus muscu
	2	1371.2	31.9	3990	11	AK085532	AK085532 Mus muscu
	3	1137.6	26.4	2521	11	AK082103	AK082103 Mus muscu
	4	1126.4	26.2	3611	11	AK085165	AK085165 Mus muscu
	5	1020	23.7	2669	11	AK076426	AK076426 Mus muscu
c	6	987	22.9	1201	9	AL571798	AL571798 AL571798
c	7	866	20.1	957	12	BI520706	BI520706 603071813
c	8	860.2	20.0	1201	9	AL553041	AL553041 AL553041
	9	851	19.8	942	9	AL543805	AL543805 AL543805
	10	848	19.7	891	13	BQ229233	BQ229233 AGENCOURT
	11	816.2	19.0	1201	9	AL546465	AL546465 AL546465
	12	808.6	18.8	972	12	BI858627	BI858627 603389094
c	13	802.4	18.7	942	9	AL570142	AL570142 AL570142
	14	794.8	18.5	884	13	BU557315	BU557315 AGENCOURT
	15	792	18.4	911	13	BQ719386	BQ719386 AGENCOURT
c	16	788	18.3	1201	9	AL571072	AL571072 AL571072
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	18	772	17.9	1201	9	AL553065	AL553065 AL553065
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	20	741.8	17.2	770	12	BM014035	BM014035 603639686
c	21	740.2	17.2	942	13	BX345882	BX345882 BX345882
	22	738	17.2	999	13	BX417121	BX417121 BX417121
	23	736	17.1	1201	9	AL545283	AL545283 AL545283
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	27	727.8	16.9	885	12	BG769122	BG769122 602743382
	28	718	16.7	785	9	AU117045	AU117045 AU117045
	29	712.8	16.6	743	9	AU138228	AU138228 AU138228
	30	708.8	16.5	961	12	BM804821	BM804821 AGENCOURT
c	31	706.2	16.4	800	9	AI760041	AI760041 wg57e06.x
	32	705	16.4	716	9	AL699988	AL699988 DKFZp686K
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c	40	673	15.6	699	12	BM974913	BM974913 UI-CF-EC1
c	41	662.6	15.4	751	9	AA651686	AA651686 nm47b02.r
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	43	659.6	15.3	726	9	AU134688	AU134688 AU134688
c	44	655.2	15.2	672	9	AA573116	AA573116 nj41e05.s
	45	652	15.2	795	13	BU600328	BU600328 AGENCOURT

ALIGNMENTS

RESULT 1

AK083415

LOCUS AK083415 3878 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030003K13 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK083415

VERSION AK083415.1 GI:26350536

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3878)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES
source Location/Qualifiers
1. .3878
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/clone="D030003K13"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"

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polyA_site         3878
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BASE COUNT        1109 a      861 c      812 g      1096 t
ORIGIN

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Matches 2665; Conservative 0; Mismatches 1043; Indels 327; Gaps 34;

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Db      64 AAACAGCAGAGCGGCTACCAGACTCTCACAGGAGCAAGCTGTAACATGCAATCGCCCGCA 123

Qy      253 AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGG 312
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Qy      313 GGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTC---CGCTTTTGCAAACCGCAGAG 369
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Db      363 --CTTCCCTCCTCCGTGCCAACGAAATATTGAGATCAGCAAGACTTTTAAATACATCAAC 420

Qy      550 ACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCCACACTTCTGAGA 609
         ||| ||||| ||||| ||||| ||||| || || ||||| ||||| || || || || ||
Db      421 ACGATTGTGTCGTGCCTCGTGTTCGTGCTAGGCATCATCGGGAACCCACGCTGCTAAGA 480

Qy      610 ATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT 669

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Db	481	ATCATCTACAAGAACAAGTGCATGCGCAATGGTCCCAATATCTTGATCGCCAGTCTGGCT	540
Qy	670	CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA	729
Db	541	CTGGGAGACCTACTGCACATCATCATAGACATACCCATTAAACACCTACAAGTTGCTCGCA	600
Qy	730	GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	789
Db	601	GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTTCT	660
Qy	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Db	661	GTGGGAATCACAGTGCTGAGTCTTTGTGCTCTAAGTATTGACAGATATCGAGCTGTTGCT	720
Qy	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Db	721	TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTA	780
Qy	910	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Db	781	ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG	840
Qy	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT	1029
Db	841	TCGGACTACAAAGGAAAGCCCCTAAGGGTCTGCATGCTTAATCCCTTTCAGAAAACAGCC	900
Qy	1030	TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAAGTTTCTATTTCTGCTTG	1089
Db	901	TTCATGCAGTTTTTACAAGACAGCCAAAGATTGGTGGCTGTTTCAAGTTTCTACTTCTGCTTG	960
Qy	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAA	1149
Db	961	CCGCTAGCCATCACTGCAGTCTTTTATACCCTGATGACCTGCGAAATGCTCAGGAAGAAG	1020
Qy	1150	AGTGGCATGCAGATTGCTTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACC	1209
Db	1021	AGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGAGAAGTGGCCAAGACA	1080
Qy	1210	GTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATT	1269
Db	1081	GTCTTCTGCCTGGTCCTCGTGTGTTGCTCTCTGTTGGCTTCCCCTTCACCTCAGCCGGATC	1140
Qy	1270	CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTG	1329
Db	1141	CTGAAGCTCACCTGTATGACCAGAGCAATCCACACAGGTGTGAGCTTCTGAGCTTTTTG	1200
Qy	1330	TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATT	1389
Db	1201	TTGGTTTTGGACTACATTGGTATCAACATGGCTTCTTTGAACTCCTGCATCAATCCAATC	1260
Qy	1390	GCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGCTGG	1449
Db	1261	GCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGTTTGTGCTGCTGG	1320
Qy	1450	TGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAA	1509

[illegible]

Qy	2342	AAAGAGAAAATAGAATGTTTGA	AAAGGCTATCCCAA	AAAGACTTTT	TTTGAATCTGT	CATT	CAC	2401
Db	2107	AAAGACACAAA-----	ACAGAA	CACTACCTATGATTTCTTTAAAGTTCTTTCAAAT				2157
Qy	2402	ATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTTT						2461
Db	2158	ATCCTTTTCATGATTGAAGTTTAAATTC	CATGTGTTCAACTTCATCA-----					2203
Qy	2462	CAC	TATCGTAGCTTAAACTCTGTTTGGTTTTGT	CATCTGTAAATACTTACCTACATACAC				2521
Db	2204	-----	TCTGTAAATACTTAGCTATTAGCTATAAGCAC					2235
Qy	2522	TGCATGTAGATGATTAAATGA--GGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGA						2579
Db	2236	TACACGTAGAGGACTTAACAAAGGGCAGGTCCCAGCGTTCGTAGCTTTCTGACAAAGAGA						2295
Qy	2580	TGCCAGTGACCTCATAAT--AAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAA						2637
Db	2296	TGCCAGTAACCCGGTTATAGACAGAAATGTGAATTGCCCGGTGCAGTGTCCACATGGCAAA						2355
Qy	2638	GGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTAT						2697
Db	2356	GAAGCAGGGAGCATC--CTTTCAGCCATGCTGTAGAGAAAATGGTCCACAGC-----AC						2407
Qy	2698	AATGCTATAGTTAAAAATACTATTTTTTCAAAATCATA	CAGATTAGT-ACATTTAACAGCTA					2756
Db	2408	AATATGATAGCGAAAATACCGTGGTTTAA	CGCCATAGAAAATAGTCACTGTAACCAAGCTC					2467
Qy	2757	CCTGTAAAGCTTATTACTAA-TTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTT						2815
Db	2468	TCTCGGAGGCATACTACCAACTTTTTTATGTTATTCTTGAAAAATAGCCAATAGAAAGGCGT						2527
Qy	2816	GCTTGACATGGTGCCTTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTTGAGACCGTAAGAAC						2875
Db	2528	TCTGGACATGGTGCCTTTTTCTAAAACGTAGAAGCCAACTGCTTCGGGGTCTGCAAGATC						2587
Qy	2876	CTCTTAGCTTTGTGCGTTTCCCTGCCTAATTTTTTATATCTTCTAAGCAAA-----						2923
Db	2588	CTCCT--CTTTGCGCATTTCTTGCTAGGTTTTTTTTTTTTTTTTTTTAACTCCTTCCACG						2645
Qy	2924	--GTGCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGA						2981
Db	2646	ACGTGCCTTAGGTTCACTCCGGATGAGCGGTGTGTGAAAGAAATGCCCAAGAGAAAACTGA						2705
Qy	2982	AGAGAGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGC						3041
Db	2706	AGAGAGAGGAAATGAGGTGGGGCCAGAGGAAGCCCGTGGGGGAAATATTCCCATTCTTAGC						2765
Qy	3042	CTAACGTTTCGTCAATGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAA						3101
Db	2766	CCTGTGTTTCGTCACTGCCACGTCAATGTCGGTGTGAAAGGTCCTGGTTCGGCTCCAGCAAA						2825
Qy	3102	ACACAGTGCAATGTTCTCAGAGTGACTTTCGAAAATAAATTGGGCCCCAAGAGCTTTAACTC						3161
Db	2826	ACAAAGCGCAGCGTTCTCAGCGTGAC-TCGGGAACAAACCAAGCCCGAGAGCTTTAAACCT						2884

Qy 3162 GGTCTTAAAATATGCCCAAATTTT----- 3185
 ||||| |||
 Db 2885 TGTCTTAAAATATAACAGATTTTCCTTCCTTCCTTTTCTCTTTCTTCTCTTCTCTC 2944

Qy 3186 -----TACTTTGTTTTTCTTTTAATAGGCTGGGCCACATG 3220
 ||| ||||| ||| |||||
 Db 2945 TTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTTTCATAACCCAGGCCACATG 3004

Qy 3221 TTGGAATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACC 3280
 ||| ||||| ||| ||| ||| ||| ||| |||||
 Db 3005 TTGAAAATGAGCTTAACAATGCAGTTTTCTACCAAATCATTGTGACAATAACAATAAACC 3064

Qy 3281 AAAACCCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGG 3340
 |||| ||||| || ||||| ||||| ||||| |||||
 Db 3065 CAAACGGGACAATGAGGTAAAAACCAAGAACAATACTGAATCCACGTGACAC----ATG 3120

Qy 3341 ATTCTATTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAG 3400
 |||| |||| ||||| ||||| ||||| |||||
 Db 3121 ACTCTCTTTAGGAGTCACCCACAGTTCTTGTGTGTA-----CAGAT 3161

Qy 3401 AGGCCTGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATT-TTGAATCACT 3459
 || ||||| ||| ||| ||||| ||||| ||||| |||||
 Db 3162 TGCTTTTTTAATCATAAAGGACGCCCCAGATCTTCAATTTTAAGTTAGTTATTGGCTCCCC 3221

Qy 3460 AATATTTTCACAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATT 3519
 || ||||| ||| ||||| ||||| ||||| ||||| |||||
 Db 3222 AGTAGTTTCACAGCGTGGATATATTTTTAATTTTA-CTAAGTTTtagattggTTTTATT 3280

Qy 3520 ACCATGTACTGAATTTTTACATCCTGATACCCTTTCCTTCTCCATGT-----CAGTA 3571
 ||| ||||| ||| ||||| ||||| ||||| |||||
 Db 3281 GTTGTGTTCTAAATTCTTAAGTCCTAACATCTTTGTTTAACCCAGATGTTCCCTTCCCTCT 3340

Qy 3572 TCATGTTCTCTAATTATCTTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCATT 3631
 |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3341 TCATGGGCAATAATCGTCCTGCCAAATTATGAAATGGCATAAGAATACTATTACATAAT 3400

Qy 3632 ATTTATAATAAAATTGCATTCACTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAA 3691
 || ||||| ||| ||||| ||||| ||||| ||||| |||||
 Db 3401 ATATACAATAAACTATATTAAGTGGCTTTTTTATTAAAAATTTTAGCACA-----CAG 3454

Qy 3692 CATACTGATAAGTAAGAAACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAA 3751
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3455 ACCAAGGGTGATAAGAAAAAAACATGATTCCCTTGCCATAATTAAACCAAGATAAGAGA 3514

Qy 3752 AGGTGCTATCGTTCAACTTCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAAC 3811
 |||| |||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3515 AGGTACCATCT--AATTTAAAGCATATTTTCTAACATTTAAGTAGCCTAATATAGCAAT 3571

Qy 3812 AGACAAAATTATTGTTAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACC 3871
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3572 GCATAAAAATAGTGTTAAACAAGGATGTTAGAGGTCAAACGATTTGTAAGTGACTTCAGCC 3631

Qy 3872 TATTTTCTCCCTTATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATT 3931
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3632 TATTTTCTCCCAAATTATTTACTGCTATTTTGGTCTGTGTTCAAACA-TTTTCAGTATT 3690

Qy 3932 GATAGCTTACATATGGCCAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCT 3991


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Db      3691 GATAATGTGCA-ACAGCCAAAGGAACACTGTTTTTCATCCAAATGCGGGTGTGTTGTACCT 3749

Qy      3992 AACTTTATAAAAGTGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTTGG 4051
      ||| | | | | | | | | | | | | | | | | | | | | | |
Db      3750 AAC---ATGCACTTGTAATAAAGCCGTGTAAAA---TAACTGTGTTTTGTTTTGCTCTGG 3803

Qy      4052 TTGCCTAAAGTGGC-----TATAGTTACTGATTTTTTTATTATGTAAGCAAAACCAATAA 4105
      | ||||| |||| | | | | | | | | | | | | | | | | |
Db      3804 TCACCTAAAGTGGCAGCTTGTGTGCTTGCTAACTTCTTGTGTTAGTAAGCAAAACCAATAA 3863

Qy      4106 AAATTTAAGTTTTTTT 4120
      | | | | | | |
Db      3864 ACGTTCAAATGGTTT 3878

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RESULT 2

AK085532

LOCUS AK085532 3990 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630038G12 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085532

VERSION AK085532.1 GI:26351656

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3990)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/

Db	417	TCCTCCGCACCTGCGGAGGTGACCAAAGGAGGGAGGGGGGCTGGAGTCCCGCCAAGATC-	475
Qy	490	ATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAAC	549
Db	476	--CTTCCCTCCTCCGTGCCAACGAAATATTGAGATCAGCAAGACTTTTAAATACATCAAC	533
Qy	550	ACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACTCCACACTTCTGAGA	609
Db	534	ACGATTGTGTCGTGCCTCGTGTTCGTGCTAGGCATCATCGGGAACTCCACGCTGCTAAGA	593
Qy	610	ATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT	669
Db	594	ATCATCTACAAGAACAAGTGCATGCGCAATGGTCCCAATATCTTGATCGCCAGTCTGGCT	653
Qy	670	CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA	729
Db	654	CTGGGAGACCTACTGCACATCATCATAGACATACCCATTAAACACTACAAGTTGCTCGCA	713
Qy	730	GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC	789
Db	714	GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGGCTTCT	773
Qy	790	GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT	849
Db	774	GTGGGAATCACAGTGTGCTGAGTCTTTGTGCTCTAAGTATTGACAGATATCGAGCTGTTGCT	833
Qy	850	TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG	909
Db	834	TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTA	893
Qy	910	ATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG	969
Db	894	ATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG	953
Qy	970	ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT	1029
Db	954	TCGGACTACAAAGGAAAGCCCCTAAGGGTCTGCATGCTTAATCCCTTTCAGAAAACAGCC	1013
Qy	1030	TTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG	1089
Db	1014	TTTCATGCAGTTTTACAAGACAGCCAAAGATTGGTGGCTGTTTCAGTTTCTACTTCTGCTTG	1073
Qy	1090	CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAA	1149
Db	1074	CCGCTAGCCATCACTGCAGTCTTTTATACCCTGATGACCTGCGAAATGCTCAGGAAGAAG	1133
Qy	1150	AGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACC	1209
Db	1134	AGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGAGAAGTGGCCAAGACA	1193
Qy	1210	GTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATT	1269
Db	1194	GTCTTCTGCCTGGTCCTCGTGTGTGCTCTCTGTTGGCTTCCCCTTCACCTCAGCCGGATC	1253
Qy	1270	CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTG	1329
Db	1254	CTGAAGCTCACCTGTATGACCAGAGCAATCCACACAGGTGTGAGCTTCTGAGCTTTTTG	1313

Qy	1330	TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCATTAACCCAATT	1389
Db	1314	TTGGTTTTGGACTACATTGGTATCAACATGGCTTCTTTGAACTCCTGCATCAATCCAATC	1373
Qy	1390	GCTCTGTATTTGGTGAGCAAAAGATTCAAAAACGCTTTAAGTCATGCTTATGCTGCTGG	1449
Db	1374	GCTCTGTATTTGGTGAGCAAAAGATTCAAAAACGCTTTAAGTCATGTTTGTGCTGCTGG	1433
Qy	1450	TGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAA	1509
Db	1434	TGCCAAACGTTTGAGGAAAAGCAGTCCTTGGAGGAGAAGCAGTCCTGCCTGAAGTTCAAA	1493
Qy	1510	GCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG	1569
Db	1494	GCCAACGATCACGGATATGACAACTTCCGTTCCAGCAATAAATACAGCTCGTCTTGAAAG	1553
Qy	1570	AAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAAAACAAAATG	1629
Db	1554	CAAGAACACTCGCCGAATCTCACTGTCCTCATTTGTGGACAGATACCATTAAAACAAAATG	1613
Qy	1630	AAACATTTGCCAAAAACAAAACAAAAAATATGTATTTGCACAGCACACTATTAAAATATT	1689
Db	1614	AAACCGTTGCCAAATCAAATGGAAAAAACCATGTAGCAGAAAGGTGTGCGCGCGTGTG	1673
Qy	1690	AAGTGTAATTATTTTAACTCAGCTACATATGAC-----ATTTTATGAGCTGTTTAC	1744
Db	1674	AGAGGGATTATTTTAACTGTTCTGACGCTCAACACCGGATATATTCACGGGCTGTTTAC	1733
Qy	1745	GGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTT	1804
Db	1734	AACCTAAGAAAGCTGTGGGAAGGAATGAAGCCCTCCTCCGTGGGAAGCACTTAGATTCT	1793
Qy	1805	TACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACTTAGG	1864
Db	1794	T--AGTCAGCACTTCAGCAGAGCTCTTAAAGCCCCTAGTGCGTTACATGCCACTTACG	1851
Qy	1865	CTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATC	1924
Db	1852	TTTAAAAA-----AACGAGAACTTCACTGAAGTTCTGTTCAGGAGTTTATTATCCAGT	1904
Qy	1925	AATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATGAAGC	1984
Db	1905	CCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAAACAATTCTTAAACGAAGTT	1962
Qy	1985	TTAAATTACTCAATTTAAATTTTAAATCCTTTAAAACAACTTTTCAATTAATATTATC	2044
Db	1963	TCAATTGCTTAATTTGAACTTAAAAAAAAAAAACTAATAAATTTTATGCATACTATC	2022
Qy	2045	--ACACTATTATCAGATTGTAATTAGATGCAAAATGAGAGAGCAGTTTAGTTGTTGCA--TT	2101
Db	2023	ATACCCACTAATCTGATTGTAACATATGCAAAAGAAAAGGCAATATGGTTGGTAAACTT	2082
Qy	2102	TTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTT	2161
Db	2083	TTTTGGTCATTACCAACATTGAAATGATCAGAAATTCGGGGGAAGAAAA-----	2122

Qy 2162 TTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAACC 2221
 Db 2130 -----AGACAGCC 2137

Qy 2222 AACATGTCAAAACAAGCAGCATGTAACAGACTGGCAGCATGTGCCAGCTGAATTTAAAT 2281
 Db 2138 TGCGAATGCCACAGAGAAAAATGGGAAAGCGTG----- 2171

Qy 2282 ATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCAC 2341
 Db 2172 -----AGCTGCTATGCCTGAGACTTCTGAAATTCCTCACACATACTCTGCAG 2219

Qy 2342 AAAGAGAAATAGAATGTTTGAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTTCAC 2401
 Db 2220 AAAGACACAAA-----ACAGAACTACCTATGATTTCTTTAAAGTTCTTTCAAAT 2270

Qy 2402 ATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTTT 2461
 Db 2271 ATCCTTTTCATGATTGAAGTTTAAATTCATGTGTTCAACTTCATCA----- 2316

Qy 2462 CACTATCGTAGCTTAAACTCTGTTTGGTGTGTCATCTGTAAATACTTACCTACATACAC 2521
 Db 2317 -----TCTGTAAATACTTAGCTATTAGCTATAAGCAC 2348

Qy 2522 TGCATGTAGATGATTAAATGA--GGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGA 2579
 Db 2349 TACACGTAGAGGACTTAACAAAGGGCAGGTCCCAGCGTTCGTAGCTTTCTGACAAAGAGA 2408

Qy 2580 TGCCAGTGACCTCATAAT--AAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAA 2637
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Qy 2638 GGGGCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTAT 2697
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Qy 2698 AATGCTATAGTTAAAATACTATTTTTCAAATCATAAGATTAGT-ACATTTAACAGCTA 2756
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Qy 2876 CTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAA----- 2923
 Db 2701 CTCCT--CTTTGCGCATTCTTGTCTAGGTTTTTTTTTTTTTTTTTAATCTCCTTCCACG 2758

Qy 2924 --GTGCCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGA 2981
 Db 2759 ACGTGCCTTAGGTTCACTCCGGATGAGCGGTGTGTGAAAGAATGCCCAAGAGAAAACCTGA 2818

Qy 2982 AGAGAGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGC 3041

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Qy	3102	ACACAGTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTC	3161
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Qy	3341	ATTCTATTTATAAATCACCCACAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAG	3400
Db	3234	ACTCTCTTTAGGAGTCACCCACAGTTCTTGTGTGTA-----CAGAT	3274
Qy	3401	AGGCCTGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATT-TTGAATCACT	3459
Db	3275	TGCTTTTTAATCATAAAGGACGCCCCAGATCTTCAATTTTAAGTTAGTTATTGGCTCCCC	3334
Qy	3460	AATATTTTACAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATT	3519
Db	3335	AGTAGTTTACAGCGTGGATATATTTTAAATTTTA-CTAAGTTTtagattggTTTTATT	3393
Qy	3520	ACCATGTACTGAATTTTTACATCCTGATACCTTTCTCTTCTCCATGT-----CAGTA	3571
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Qy	3572	TCATGTTCTCTAATTATCTTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCATT	3631
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Qy	3692	CATACTGATAAGTAAGAAACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAA	3751
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Db	3977 ACGTTCAAATGGTT 3990	

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2521)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

Qy 370 ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG 429
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 Db 348 GTAATGACGCCACCCACTAAGACCTCCTGGACCAGAGGTTCCAACCTCAGTCTGATGCGT 407

Qy 430 TCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACC 489
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 Db 825 TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTA 884

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Qy 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT 1029
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 Db 945 TCGGACTACAAAGGAAAGCCCCTAAGGGTCTGCATGCTTAATCCCTTTCAGAAAACAGCC 1004

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 Db 1125 AGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGAGAAGTGGCCAAGACA 1184

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Db	1185	GTCTTCTGCGCTGGTCCCTCGTGTCTTGCTCTCTGTTGGCTTCCCCTTCACCTCAGCCGGATC	1244
Qy	1270	CTGAAGCTCACTCTTTATAAATCAGAAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTG	1329
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Qy	1510	GCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG	1569
Db	1485	GCCAACGATCACGGATATGACAACTTCCGGTCCAGCAATAAATACAGCTCGTCTTGAAGG	1544
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Db	1545	CAAGAACTCTGCCGAATCTCACTGTCTCATTTGTGGACAGATACCATTAAAAACAAAATG	1604
Qy	1630	AAACATTTGCCAAAAACAAAAACAAAACTATGTATTTTGCACAGCACACTATTAAAAATATT	1689
Db	1605	AAACCGTTGCCAAATCAAAATGGAAAAAACCATGTAGCAGAAAAGGTGTGCGCGGTGTG	1664
Qy	1690	AAGTGTAAATTATTTTAACTCACAGCTACATATGACAT-----TTTATGAGCTGTTTAC	1744
Db	1665	AGAGGGATTATTTTAACTGTTCTGACGCTCAACACCGGATATATTACGGGCTGTTTAC	1724
Qy	1745	GGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTTT	1804
Db	1725	AACCTAAGAAAGCTGTGGGAAGGAATGAAGCCCTCCTCCGTGGGGAAGCACTTAGATTCT	1784
Qy	1805	TACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACTTAGG	1864
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RESULT 4

AK085165

LOCUS AK085165 3611 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430047G06 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085165

VERSION AK085165.1 GI:26351484

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

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AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

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AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,

Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3611)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES
source Location/Qualifiers
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PRECURSOR (SWISSPROT|P48302, evidence: FASTY, 100%ID,  
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ORIGIN

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Qy	1923	TCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAAGAACTTTTAAATGAA	1982
Db	1900	GTCCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAAACAATTCTTAAACGAAG	1957
Qy	1983	GCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAAAACAACCTTTTCAATTAATATTA	2042
Db	1958	TTTCAATTGCTTAATTTGAACTTAAAAAAAAAAAACTAATAAATTTTATGCATACTA	2017
Qy	2043	TC--ACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCA-	2099
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Db	2169	-----AGCTGCTATGCCTGAGACTTCTGAAATTCCCTCACACATACTCTGC	2214
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Db 2215 AGAAAGACACAAA-----ACAGAACTACTACCTATGATTTCTTTAAAGTTCTTTCAA 2265

Qy 2400 ACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTT 2459
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Db 2266 ATATCCTTTTCATGATTGAAGTTTAAATTCCATGTGTTCAACTTCATCA----- 2313

Qy 2460 TTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAATACTTACCTACATAC 2519
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Db 2314 -----TCTGTAAATACTTAGCTATTAGCTATAAGC 2343

Qy 2520 ACTGCATGTAGATGATTAAATGA--GGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGA 2577
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Db 2344 ACTACACGTAGAGGACTTAACAAAGGCAGGTCCCAGCGTTCGTAGCTTTCTGACAAAGA 2403

Qy 2578 GATGCCAGTGACCTCATAAT--AAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACA 2635
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Db 2404 GATGCCAGTAACCCGGTTATAGACAGAATGTGAATTGCCCGGTGCAGTGTCCACATGGCA 2463

Qy 2636 AAGGGGCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGT 2695
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Db 2464 AAGAAGCAGGGAGCATC--CTTTCAGCCATGCTGTAGAGAAAATGGTCCACAGC----- 2515

Qy 2696 ATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGT-ACATTTAACAGC 2754
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Db 2516 ACAATATGATAGCGAAAATACCGTGGTTTAAACGCATAGAAAATAGTCACTGTAACCAGC 2575

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Qy 3068 TCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGAC 3127
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Qy      3184 -----TTT 3186
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Qy      3367 TTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT 3426
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RESULT 5

AK076426

LOCUS AK076426 2669 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832401B07 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK076426

VERSION AK076426.1 GI:26345371

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
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 Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
 Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
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 Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
 Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
 Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
 Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
 Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
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 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
 and Hayashizaki,Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 2669)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .2669 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:4832401B07" /db_xref="taxon:10090" /clone="4832401B07" /tissue_type="head" /clone_lib="RIKEN full-length enriched mouse cdNA library" /dev_stage="0 day neonate"

CDS 220. .1548 /note="unnamed protein product; ENDOTHELIN B RECEPTOR PRECURSOR (SWISSPROT|P48302, evidence: FASTY, 100%ID, 100%length, match=1326) putative" /codon_start=1 /protein_id="BAC36337.1" /db_xref="GI:26345372" /translation="MQSPASRCGRALVALLACGFLGVWGEKRGFPAPAQATLSLLGTK EVMTPTTKTSWTRGSNSSLMRSSAPAEVTKGGRGAGVPPRSFPPPCQRNIEISKTFKY INTIVSCLVFVLGIIGNSTLLRIIYKNKCMRNGPNILIASLALGDLHLIIIDIPINTY KLLAEDWPFGAEMCKLVPFIQKASVGITVLSLCALSIDRYAVASWSRIKGIGVPKWT AVEIVLIWVSVVLAVPEAIGFDMITS DYKKGKPLRVCM LNPFQKTA FMQFYKTAKDWW LFSFYFCLPLAITAVFYTLMTCEMLRKKSGMQIALNDHLKQRREVAKTVFCLVLVFAL CWLPLHLSRIILKLTLYDQSNPHRCELLSFLLVLDYIGINMASLNSCINPIALYLVSKR FKNCFKSCLCWCQTFEKQSLEEKQSCLKFKANDHGYDNFRSSNKYSSS"

BASE COUNT 714 a 613 c 593 g 749 t

ORIGIN

Query Match 23.7%; Score 1020; DB 11; Length 2669;
Best Local Similarity 84.7%; Pred. No. 1.4e-134;
Matches 1169; Conservative 0; Mismatches 205; Indels 6; Gaps 2;

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Db      175 AAACAGCAGAGCGGCTACCAGACTCTCACAGGAGCAAGCTGTAACATGCAATCGCCCGCA 234

Qy      253 AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGG 312
        || | ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| ||
Db      235 AGCCGGTGCGGACGCGCCTTGGTGGCGCTGCTGCTGGCCTGTGGCTTCTTGGGGGTATGG 294

Qy      313 GGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTC---CGCTTTTGCAAACCGCAGAG 369
        ||||| || ||||| ||||| ||||| ||||| || ||||| || ||||| ||
Db      295 GGAGAGAAAAGAGGATTCCACCTGCCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG 354

Qy      370 ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG 429
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      355 GTAATGACGCCACCCACTAAGACCTCCTGGACCAGAGGTTCCAACCTCAGTCTGATGCGT 414

Qy      430 TCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACC 489
        || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      415 TCCTCCGCACCTGCGGAGGTGACCAAGGAGGGAGGGGGGCTGGAGTCCCGCCAAGATC- 473

Qy      490 ATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAAC 549
        || ||||| ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||
Db      474 --CTTCCCTCCTCCGTGCCAACGAAATATTGAGATCAGCAAGACTTTTAAATACATCAAC 531

Qy      550 ACGGTTGTGTCCTGCCTTGTGTTGCTGCTGGGGATCATCGGGAACTCCACACTTCTGAGA 609
        ||| ||||| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||
Db      532 ACGATTGTGTCGTGCCTCGTGTTGCTGCTAGGCATCATCGGGAACTCCACGCTGCTAAGA 591

Qy      610 ATTATCTACAAGAACAAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT 669
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      592 ATCATCTACAAGAACAAAGTGCATGCGCAATGGTCCCAATATCTTGATCGCCAGTCTGGCT 651

Qy      670 CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA 729
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      652 CTGGGAGACCTACTGCACATCATCATAGACATACCCATTAAACACCTACAAGTTGCTCGCA 711

Qy      730 GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      712 GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAGGCTTCT 771

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      772 GTGGGAATCACAGTGCTGAGTCTTTGTGCTCTAAGTATTGACAGATATCGAGCTGTTGCT 831

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      832 TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTTA 891

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      892 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG 951

Qy      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAAGACAGCT 1029
```

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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      952 TCGGACTACAAAGGAAAGCCCCTAAGGGTCTGCATGCTTAATCCCTTTAGAAAACAGCC 1011
Qy      1030 TTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTAGTTTTCTATTTCTGCTTG 1089
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1012 TTCATGCAGTTTTACAAGACAGCCAAAGATTGGTGGCTGTTAGTTTTCTACTTCTGCTTG 1071
Qy      1090 CCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAA 1149
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1072 CCGCTAGCCATCACTGCAGTCTTTTATACCCTGATGACCTGCGAAATGCTCAGGAAGAAG 1131
Qy      1150 AGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACC 1209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1132 AGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGAGAAGTGGCCAAGACA 1191
Qy      1210 GTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATT 1269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1192 GTCTTCTGCCTGGTCCTCGTGTGCTCTGTTGGCTTCCCCTTCACCTCAGCCGGATC 1251
Qy      1270 CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTGAGCTTTCTG 1329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1252 CTGAAGCTCACCTGTATGACCAGAGCAATCCACACAGGTGTGAGCTTCTGAGCTTTTTTG 1311
Qy      1330 TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATT 1389
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1312 TTGGTTTTGGACTACATTGGTATCAACATGGCTTCTTTGAACTCCTGCATCAATCCAATC 1371
Qy      1390 GCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGG 1449
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1372 GCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGTTTGTGCTGCTGG 1431
Qy      1450 TGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA 1509
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1432 TGCCAAACGTTTGAAGAAAAGCAGTCCTTGGAGGAGAAGCAGTCCTGCCTGAAGTTCAA 1491
Qy      1510 GCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG 1569
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Db      1492 GCCAACGATCACGGATATGACAACCTCCGGTCCAGCAATAAATACAGCTCGTCTTGAAG 1551

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RESULT 6

AL571798/c

LOCUS AL571798 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL571798 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI030YM19 3-PRIME, mRNA sequence.

ACCESSION AL571798

VERSION AL571798.2 GI:31293189

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 16, 2001 this sequence version replaced gi:12929453.

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7006.r For
 more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI030AG10NP1&cluster=7006.r)
[cgi-bin/cluster.cgi?seq=CS0DI030AG10NP1&cluster=7006.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI030AG10NP1&cluster=7006.r). Contact :
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI030AG10NP1.

FEATURES
 source Location/Qualifiers
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI030YM19"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 331 a 259 c 269 g 299 t 43 others
 ORIGIN

Query Match 22.9%; Score 987; DB 9; Length 1201;
 Best Local Similarity 96.0%; Pred. No. 7.8e-130;
 Matches 1030; Conservative 10; Mismatches 28; Indels 5; Gaps 3;

Qy	489	CATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAA	548
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Db	1068	CMCATCTCCCYCCCCCGTGCCAAGACCCATCGAGATCAAG--AGAYTTCAAATACATCAA	1011
Qy	549	CACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAG	608
		: : :	
Db	1010	CAC-GTTKTKTCCTGCCTTGTGTTTCGTGCTGGGATCATC--GGRACCTCCACACTTCTGAG	954
Qy	609	AATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGC	668
Db	953	AATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGC	894
Qy	669	TCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGC	728
Db	893	TCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGC	834
Qy	729	AGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTC	788
Db	833	AGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTC	774
Qy	789	CGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGC	848
Db	773	CGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGC	714
Qy	849	TTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTT	908

Db	713	TTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTTT	654
Qy	909	GATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTAC	968
Db	653	GATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTAC	594
Qy	969	GATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGC	1028
Db	593	GATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGC	534
Qy	1029	TTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTT	1088
Db	533	TTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTATTTCTGCTT	474
Qy	1089	GCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAA	1148
Db	473	GCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAA	414
Qy	1149	AAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAAC	1208
Db	413	AAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAAC	354
Qy	1209	CGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGGAT	1268
Db	353	CGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGGAT	294
Qy	1269	TCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCT	1328
Db	293	TCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCT	234
Qy	1329	GTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAAT	1388
Db	233	GTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAAT	174
Qy	1389	TGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTG	1448
Db	173	TGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTG	114
Qy	1449	GTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA	1508
Db	113	GTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA	54
Qy	1509	AGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCAT	1561
Db	53	AGCTAATGATNANNGATATGACAACTTCCGTTCCAGKNNBNBGTSCAGCKCVT	1

RESULT 7

BI520706/c

LOCUS	BI520706	957 bp	mRNA	linear	EST 29-AUG-2001
DEFINITION	603071813T1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163746 3', mRNA sequence.				
ACCESSION	BI520706				
VERSION	BI520706.1 GI:15345498				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 957)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Life Technologies, Inc.
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM11406 row: j column: 03
                High quality sequence start: 4
                High quality sequence stop: 954.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_119"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.3 kb, insert size range
                     0.9-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 013. Note:
                     this is a NIH_MGC Library."
BASE COUNT        289 a      225 c      199 g      244 t
ORIGIN

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Db 777 CTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGA 718

Qy 809 GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAG 868
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Db 717 GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAG 658

Qy 869 GAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCTCTGTGG 928
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Db 657 GAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCTCTGTGG 598

Qy 929 TTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAGGAAGTT 988
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Db 597 TTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAGGAAGTT 538

Qy 989 ATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTTACAAGA 1048
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Db 537 ATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTTACAAGA 478

Qy 1049 CAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT 1108
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Db 477 CAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT 418

Qy 1109 TT-TTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT 1167
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Db 417 TTGTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT 358

Qy 1168 TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT 1227
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Db 357 TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT 298

Qy 1228 GTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTAT 1287
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Db 297 GTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTAT 238

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Db 237 AATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATT 178

Qy 1348 GGTATCAACATGGCTTCACTGAATTCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 1407
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Db 177 GGTATCAACATGGCTTCACTGAATTCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 118

Qy 1408 AAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCT-GCTGGTGCCAGTCATTTGAAGA 1466
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Db 117 AAAAGATTCAACAAGTCTTTAAGTCATGCTTATGCTGGCTGGTGCCAGTCATTTGAAGA 58

Qy 1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATG 1516
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Db 57 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTTACAGCTAAGG 8

RESULT 8

AL553041/c

LOCUS AL553041 1201 bp mRNA linear EST 31-MAY-2003
 DEFINITION AL553041 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0DI072YK22 3-PRIME, mRNA sequence.
 ACCESSION AL553041

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VERSION      AL553041.2   GI:31274855
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 1201)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished
COMMENT      On Feb 15, 2001 this sequence version replaced gi:12892503.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 7006.r For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CS0DI072BF11NP1&cluster=7006.r. Contact :
              Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0DI072BF11NP1.

FEATURES             Location/Qualifiers
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                       /note="1st strand cDNA was primed with a NotI-oligo(dT)
                       primer. Five prime end enriched, double-strand cDNA was
                       digested with Not I and cloned into the Not I and EcoR V
                       sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      428 a      102 c      202 g      394 t      75 others
ORIGIN

Query Match      20.0%; Score 860.2; DB 9; Length 1201;
Best Local Similarity 89.9%; Pred. No. 6.2e-112;
Matches 966; Conservative 32; Mismatches 54; Indels 22; Gaps 7;

Qy      3179 AAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAA 3238
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Db      1061 AAATCCMAAATTAMCTTTTTTYTTTAAWGWKCKGKCCACWTKKRRAAAK-----CTWKA 1007

Qy      3239 TGTGTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGC 3298
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Db      1006 AATTTKTTTCTTCCAATATTAATTTT-----TTTACATAAACCAAACCAACAATTTKCC 952

Qy      3299 CAGAAAGAAAGAGCAATAATAATTAATTCACACCCATATGGATTCTATTTATAAATCAC 3358
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Db      951 ATAAAKTAA--KKTCAWTATWATTAATTCACMCMCCATATKTATYCTATTTATAAATCAC 894

Qy      3359 CCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTATCATAGAA 3418
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Db      893 CCACAWACTTKTTCTTTAATTCMWTCCTCAATCACTTTTTTCAGAGKCTGTATCATAGAA 834

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Qy 3419 GTCATTTTAGACTCTCAATTTTAAATT-AATTTTGAATCACTAATATTTTACAGTTTAT 3477
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 Db 833 GTCATTTTAGACTCTCAATTTTAAATTAAATTTTGAATCACTAATATTTTACAGTTTAT 774

Qy 3478 TAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTT 3537
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 Db 773 TAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTT 714

Qy 3538 ACATCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAA 3597
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 Db 713 ACATCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAA 654

Qy 3598 TTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGG 3657
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 Db 653 TTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATCGCATTTCAGTGG 594

Qy 3658 CTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTAT 3717
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 Db 593 CTTTTT-AAAAAATGTTTGATTCAAACTTTTACATACTGATAAGTAAGAAACAATTAT 535

Qy 3718 AATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACA 3777
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 Db 534 AATTTCTTNACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACA 475

Qy 3778 TGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATG 3837
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 Db 474 TGTTTCCTAGTATTAAGGACTTTAATATVGCACAGACAAAATTATTGTTAACATGGATG 415

Qy 3838 TTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCT 3897
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 Db 414 TTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCT 355

Qy 3898 AATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAAT 3957
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 Db 354 AATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAAT 295

Qy 3958 ACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAA 4017
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 Db 294 ACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAA 235

Qy 4018 TGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 4077
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 Db 234 TGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 175

Qy 4078 TTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTT-AACAACTACCTTATT 4136
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 Db 174 TTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTCAACAACTACCTTATT 115

Qy 4137 TTTCACTGTACAGACACTAATTCATTAAATACTAA-----TTGATTGTTTAAAAGAAA 4189
 |||
 Db 114 TTTCACTGTACAGACACTAATTCATTAAATACTCACACTCTCGCACTTGTTTAAAAGAAA 55

Qy 4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 4243
 ||| : |||
 Db 54 TATAAAKGBGMCAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 1

AL543805

DEFINITION AL543805 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YG20 5-PRIME, mRNA sequence.

VERSION AL543805.2 GI:31265651

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 942)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 15, 2001 this sequence version replaced qi:12876284.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7006.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0DI005BD10QP1&cluster=7006.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI005BD10QP1.

FEATURES	Location/Qualifiers
----------	---------------------

source

1. .942

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/organism="Homo sapiens"
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/mol type="mRNA"
```

```
/db xref="taxon:9606"
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/clone="CS0DI005YG20"
```

```
/tissue type="PLACENTA COT 25-NORMALIZED"
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.

BASE COUNT	318 a	176 c	155 g	284 t	9 others
------------	-------	-------	-------	-------	----------

ORIGIN

Query Match 19.8%; Score 851; DB 9; Length 942;

Best Local Similarity 98.1%; Pred. No. 1.3e-110;

Matches 876; Conservative 4; Mismatches 11; Indels 2; Gaps 2;

Qy 1803 TTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTACACAACACTTA 1862

Db 51 TTCCCGGGATGCACTTCAACATAGCTCTTAACAACCTTCCAGGATATTCAACAACACTTA 110

Qy 1863 GGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAA 1922
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 111 GGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA 170


```

5', mRNA sequence.
ACCESSION      BQ229233
VERSION        BQ229233.1  GI:20410633
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 891)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: ATCC/DCTD/DTP
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM13315 row: e column: 17
                High quality sequence stop: 696.

FEATURES             Location/Qualifiers
     source            1..891
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:6055288"
                        /tissue_type="melanotic melanoma"
                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NIH_MGC_72"
                        /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                        Average insert size 2 kb. Library constructed by Life
                        Technologies."

BASE COUNT        291 a      162 c      155 g      283 t
ORIGIN

Query Match          19.7%; Score 848; DB 13; Length 891;
Best Local Similarity 99.1%; Pred. No. 3.6e-110;
Matches 884; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY      2086 GTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG 2145
          |||
Db      1 GTTTAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG 60

QY      2146 AAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCAT 2205
          |||
Db      61 AAAGAGCAAGGCTGTTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCAT 120

QY      2206 TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGTC 2265
          |||
Db      121 TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGTC 180

QY      2266 CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAAATTATTACATCCTTTACATTTCAGT 2325
          |||

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Db      181 CAGCTGAATTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT 240
Qy      2326 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAAGACTTTTTT 2385
        |||
Db      241 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAAGACTTTTTT 300
Qy      2386 TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT 2445
        |||
Db      301 TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT 360
Qy      2446 TAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAAT 2505
        |||
Db      361 TAAAATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTGTCATCTGTAAAT 420
Qy      2506 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 2565
        |||
Db      421 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 480
Qy      2566 TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCAGTGT 2625
        |||
Db      481 TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCAGTGT 540
Qy      2626 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTC 2685
        |||
Db      541 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCTATGCTGTGGTTAAATGGTTTC 600
Qy      2686 TAGCATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACA 2745
        |||
Db      601 TAGCATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACA 660
Qy      2746 TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 2805
        |||
Db      661 TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 720
Qy      2806 AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGC-AAAAGTCTTTTGTAG 2864
        |||
Db      721 AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGC-AAAAGTCTTTTGTAG 780
Qy      2865 ACCGTAAGAACCCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAG 2924
        |||
Db      781 ACCGTAAGAACCCTCTTACCTTTGTGCGTTCCTGCCTAA-TTTTAAATCTTCTAAGCAAAG 839
Qy      2925 TGCCTTAGGATAGCTTGGG-ATGAGATGTGTGTGAAAGTATGTACAAGAGAA 2975
        |||
Db      840 TGCCTTAGGATAGCTTGGGAATGAGATGTGTGTGAAAATATGTACAAGAAAA 891

```

RESULT 11

AL546465

LOCUS AL546465 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL546465 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI030YM19 5-PRIME, mRNA sequence.

ACCESSION AL546465

VERSION AL546465.2 GI:31268299

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1201)
AUTHORS        Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished
COMMENT        On Feb 15, 2001 this sequence version replaced gi:12879606.
                Contact: Genoscope
                Genoscope - Centre National de Sequencage
                BP 191 91006 EVRY cedex - France
                Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                Library was constructed by Life Technologies, a division of
                Invitrogen. This sequence belongs to sequence cluster 7006.r For
                more information about this cluster, see
                http://www.genoscope.cns.fr/
                cgi-bin/cluster.cgi?seq=CS0DI030AG10QP1&cluster=7006.r. Contact :
                Feng Liang Email : fliang@lifetech.com URL :
                http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                Faraday Avenue Genoscope sequence ID : CS0DI030AG10QP1.

FEATURES             Location/Qualifiers
     source            1. .1201
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CS0DI030YM19"
                        /tissue_type="PLACENTA COT 25-NORMALIZED"
                        /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                        /note="1st strand cDNA was primed with a NotI-oligo(dT)
                        primer. Five prime end enriched, double-strand cDNA was
                        digested with Not I and cloned into the Not I and EcoR V
                        sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT        272 a      289 c      321 g      289 t      30 others
ORIGIN

      Query Match          19.0%;   Score 816.2;   DB 9;   Length 1201;
      Best Local Similarity 97.2%;   Pred. No. 1e-105;
      Matches 854;   Conservative 7;   Mismatches 15;   Indels 3;   Gaps 3;

Qy      178  TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
Db      219  TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 278

Qy      238  ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
Db      279  ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 338

Qy      298  CTGTGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357
      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
Db      339  CTGTGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 398

Qy      358  CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417
      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
Db      399  CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 458

Qy      418  AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477
      ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
Db      459  AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 518

```

Qy 478 CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537
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 Db 519 CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 578
 Qy 538 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAGTCC 597
 |||
 Db 579 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAAGTCC 638
 Qy 598 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 657
 |||
 Db 639 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 698
 Qy 658 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 717
 |||
 Db 699 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 758
 Qy 718 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 777
 |||
 Db 759 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 818
 Qy 778 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 837
 |||
 Db 819 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 878
 Qy 838 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 897
 |||
 Db 879 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTT-CAAAATGGACAGCAGTA 937
 Qy 898 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTT 957
 |||: |||
 Db 938 GAAATTGTTTTKATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTVTT 997
 Qy 958 GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT 1017
 |||: |||: |||
 Db 998 GATATAATTACGATGGACTACAAAGG-AGTTATCTGCGAATCTGCTTGCTT-MWCCCSGT 1055
 Qy 1018 CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAA 1056
 :||| |||: |||
 Db 1056 YARAAGAAAGCTTTCATGCAGTTTTACAAAAMAGCAAAA 1094

RESULT 12

BI858627

LOCUS BI858627 972 bp mRNA linear EST 10-OCT-2001

DEFINITION 603389094F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5398054 5', mRNA sequence.

ACCESSION BI858627

VERSION BI858627.1 GI:15999374

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 972)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12014 row: 1 column: 23
High quality sequence stop: 899.

FEATURES
source Location/Qualifiers
1. .972
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5398054"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 230 a 241 c 244 g 256 t 1 others
ORIGIN

Query Match 18.8%; Score 808.6; DB 12; Length 972;
Best Local Similarity 96.3%; Pred. No. 1.3e-104;
Matches 903; Conservative 0; Mismatches 25; Indels 10; Gaps 7;

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Qy      321 GAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCC 380
        |||
Db       1 GAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCC 60

Qy      381 ACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTGCTTGGCACC 440
        |||
Db       61 ACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTGCTTGGCACC 120

Qy      441 TGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCC 500
        |||
Db      121 TGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCC 180

Qy      501 CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTC 560
        |||
Db      181 CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTC 240

Qy      561 CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAATTATCTACAA 620
        |||
Db      241 CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAATTATCTACAA 300

Qy      621 GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 680
        |||
Db      301 GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 360
```

Qy 681 GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 740
 |||
 Db 361 GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 420

Qy 741 ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCAC 800
 |||
 Db 421 ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCAC 480

Qy 801 TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 860
 |||
 Db 481 TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 540

Qy 861 AATTAAAGGAA-TTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGG 919
 |||
 Db 541 AATTAAAGGAACTTGGGGTTCCAAAATGGACAGCAGTAGAAATCG-TTTGATTTGGGTGG 599

Qy 920 TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACA 979
 |||
 Db 600 TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGG-TTTGATATAATTACGATGGACTACA 658

Qy 980 AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTGAGAGACAGCTTTTCATGCAGT 1039
 |||
 Db 659 AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTGAGAGACAGCTTTTCATGCAGT 718

Qy 1040 TTTACAAGACAGCAAAAGATTGGT-GGCTGTTTCTGCTTCTGCTTGCCATT-GGC 1097
 |||
 Db 719 TTTACAAGACAGCAAAAGATTGGTGGGCTATTTCAGTTTCTGCTTCTGCTTGCCATNGGGG 778

Qy 1098 CATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCAT 1157
 |||
 Db 779 CATCACTGCATTTTTTTTATACACTAATGACCTGTGACATGTTGAGAACGAACAGTGGCTT 838

Qy 1158 GCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTG 1217
 |||
 Db 839 GCAGAT--GCTTTAATGATCACCTAAAGCAGAGACGGAA--GTGGCAAAACCGTCTTTTG 893

Qy 1218 CCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTC 1255
 |||
 Db 894 CCTGGTCCCTGTCTTTGCCCTCTGCTGGGTTCCTTAC 931

RESULT 13

AL570142/c

LOCUS AL570142 942 bp mRNA linear EST 31-MAY-2003

DEFINITION AL570142 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YG20 3-PRIME, mRNA sequence.

ACCESSION AL570142

VERSION AL570142.2 GI:31291568

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 942)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

[illegible]

BU557315

Qy 703 CCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAG 762
 |||
 Db 360 CCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAG 419

Qy 763 CTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTG 822
 |||
 Db 420 CTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTG 479

Qy 823 AGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCA 882
 |||
 Db 480 AGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCA 539

Qy 883 AAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCT 942
 |||
 Db 540 AAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCT 599

Qy 943 GAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGC 1002
 |||
 Db 600 GAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGC 659

Qy 1003 TTGCTTCATCCCGTTTCTGCTTGCCATTGGCCATCACTGCATTTTTTATACACTA 1062
 |||
 Db 660 TTGCTTCATCCCGTTTCTGCTTGCCATTGGCCATCACTGCATTTTTTATACACTA 719

Qy 1063 TGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTATACACTA 1122
 |||
 Db 720 TGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTATACACTA 779

Qy 1123 ATGACCTGTGAAATGTT-GAGAAAGAAAAGTGGCATGCAGATTG--CTTTAAATGATCAC 1179
 |||
 Db 780 ATGACCTGTGAAATGTTGGAGAAGGAAAAGTGGCATGCCAGATGGCCTTTAAATGATCAC 839

Qy 1180 CTAAAGCAGAGA 1191
 |||
 Db 840 CCTAAAGCAAGA 851

RESULT 15

BQ719386

LOCUS BQ719386 911 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT_8469884 Lupski_sympathetic_trunk Homo sapiens cDNA clone
 IMAGE:6195994 5', mRNA sequence.

ACCESSION BQ719386

VERSION BQ719386.1 GI:21858283

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 911)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13603 row: 1 column: 11
 High quality sequence stop: 606.

FEATURES
 source Location/Qualifiers
 1. .911
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6195994"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sympathetic trunk"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGCGTCCG-3' and
 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

BASE COUNT 273 a 181 c 167 g 289 t 1 others
 ORIGIN

Query Match 18.4%; Score 792; DB 13; Length 911;
 Best Local Similarity 95.6%; Pred. No. 2.9e-102;
 Matches 859; Conservative 0; Mismatches 31; Indels 9; Gaps 4;

Qy	2310	ATCCTTTACATTTCAGTTAAGATCAAACCTCACAAGAGAAATAGAATGTTTGAAGGCTA	2369
Db	1	ATCCTTTACATTTCAGTTAAGATCAAACCTCACAAGAGAAATAGAATGTTTGAAGGCTA	60
Qy	2370	TCCCAAAGACTTTTTTGAATCTGTCTATTACATACCCTGTGAAGACAATACTATCTACA	2429
Db	61	TCCCAAAGACTTTTTTGAATCTGTCTATTACATACCCTGTGAAGACAATACTATCTACA	120
Qy	2430	ATTTTTTCAGGATTATTAATACTCTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGT	2489
Db	121	ATTTTTTCAGGATTATTAATACTCTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGT	180
Qy	2490	TTTGTCTCTGTAAATACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGG	2549
Db	181	TTTGTCTCTGTAAATACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGG	240
Qy	2550	CCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAA	2609
Db	241	CCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAA	300
Qy	2610	CTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGTAGCACCTCTCTACCCATGCTG	2669

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Db      301  |||||CTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTG 360
Qy      2670 TGGTTAAAATGGTTTCTAGCATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAT 2729
Db      361  |||||TGGTTAAAATGGTTTCTAGCATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAT 420
Qy      2730 CATACAGATTAGTACATTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATT 2789
Db      421  |||||CATACAGATTAGTACATTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATT 480
Qy      2790 TTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCA 2849
Db      481  |||||TTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCA 540
Qy      2850 AAAGTGCCTTTTGTAGACCGTAAGAACCTCTTAGCTTTGTGCGTTCTGCCTAATTTTTAT 2909
Db      541  |||||AAAGTGCCTTTTGTAGACCGTAAGAACCTCTTAGCTTTGTGCGTTCTGCCTAATTTTTAT 600
Qy      2910 ATCTTCTAAGCAAAGTGCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACA 2969
Db      601  |||||ATCTTCTAAGCAAAGTGCCTTANGATAGCTTGCATGAGATGTGTGTGAAAGTATGTACA 660
Qy      2970 AGAGAAAACGGAAGAGAGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATT 3029
Db      661  |||||AGAGAAAACGGAAGAGAGAGGAAATGACGTGGGGTTGGAGGACACCCATGGGGACAGATT 720
Qy      3030 CCCATTCTTAGCCTAACGTTTCGTTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTT 3089
Db      721  |||||CCCATTCTTAGCCTAACGTTTCGTTCATTGCCTCCGTACATCAATGGCAAAGCCCTGATTT 780
Qy      3090 TGTTCCAGCAAAACACAGTGCAAT-GTTCTCAGAGTGA-CTTTCGAAATAAATTGGGCCC 3147
Db      781  |||||TGTTCCCGCAAAACACAGTGCAATGGTTCTCAGAGTGACCTTTCAAATAAATTGGGCCC 840
Qy      3148 AAGAGCTTTAA---CTCGGTCTTAAATATG---CCCAAATTTTACTTTGTTTTTCT 3199
Db      841  |||||CAGAAGCTTTAACCTCCAGCCCTTAAATATGGACCCCAAATTTTACTTTTGTTTTT 899

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Search completed: December 12, 2003, 23:52:09
Job time : 7779.55 secs